

GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: December 22, 2005, 00:16:14 ; Search time 983 Seconds
(without alignments)
4382.854 Million cell updates/sec

Title: US-09-857-581B-66

Sequence: 1 MLELALGLXVLAIFYHLRP.....ASGLVCPLARIGVASKLS 521

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=alp
-O=/cgnt2_1/USPTO.epool_p/US09857581/runat_15122005_083138_19431/app_query.fasta_1.711
-DB=Published Applications NA_Main -QPM=fastlap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09857581 @CGN_1_1_1549 @runat_15122005_083138_19431
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA_Main:

- 1: /cgnt2_6/ptodata/1/pubna/US07_PUBCOMB.seq:*
- 2: /cgnt2_6/ptodata/1/pubna/US08_PUBCOMB.seq:*
- 3: /cgnt2_6/ptodata/1/pubna/US09_PUBCOMB.seq:*
- 4: /cgnt2_6/ptodata/1/pubna/US09B_PUBCOMB.seq:*
- 5: /cgnt2_6/ptodata/1/pubna/US10A_PUBCOMB.seq:*
- 6: /cgnt2_6/ptodata/1/pubna/US10B_PUBCOMB.seq:*
- 7: /cgnt2_6/ptodata/1/pubna/US10C_PUBCOMB.seq:*
- 8: /cgnt2_6/ptodata/1/pubna/US10D_PUBCOMB.seq:*
- 9: /cgnt2_6/ptodata/1/pubna/US10E_PUBCOMB.seq:*
- 10: /cgnt2_6/ptodata/1/pubna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2258	94.5	1756	6	US-10-171-174A-9*
2	2258	94.5	1756	6	US-10-104-706-1*
3	2256	94.4	1709	6	US-10-310-154-367
4	2256	94.4	1709	6	US-10-732-923-309
5	2250	94.2	1824	7	US-10-659-755-1
6	2248	94.1	1567	9	US-10-505-145-3
7	2130	89.2	1974	8	US-10-739-930-3497
8	944.5	39.5	1730	6	US-10-411-115-3

9	944.5	39.5	1730	8	US-10-411-225-3	Sequence 3, Appli
10	943.5	39.5	1724	6	US-10-411-115-1	Sequence 1, Appli
11	943.5	39.5	1724	6	US-10-411-225-1	Sequence 1, Appli
12	921.5	38.6	1770	8	US-10-411-115-7	Sequence 7, Appli
13	921.5	38.6	1770	8	US-10-411-225-7	Sequence 7, Appli
14	919.5	38.5	1841	7	US-10-424-599-6882	Sequence 6882, Ap
15	877.5	36.7	1328	7	US-10-424-599-78567	Sequence 78567, A
16	870	36.4	1842	7	US-10-424-599-102588	Sequence 102588,
17	843	35.3	1806	7	US-10-424-599-101968	Sequence 101968,
18	807.5	33.8	1740	7	US-10-437-963-48274	Sequence 48274, A
19	761.5	31.9	1650	7	US-10-437-963-21012	Sequence 21012, A
20	730.5	30.6	1893	7	US-10-437-963-67133	Sequence 67133, A
21	717	30.0	2278	7	US-10-424-599-100510	Sequence 100510,
22	701.5	29.4	1719	7	US-10-424-599-115417	Sequence 115417,
23	693	29.0	1308	7	US-10-260-238-1284	Sequence 1284, Ap
24	691.5	28.9	1825	7	US-10-425-114-24949	Sequence 24949, A
25	680.5	28.5	1915	8	US-10-425-115-89837	Sequence 89837, A
26	680.5	28.5	2233	8	US-10-739-930-2248	Sequence 2248, Ap
27	666.5	27.9	1930	8	US-10-425-115-94744	Sequence 94744, A
28	657	27.5	1630	7	US-10-437-963-38374	Sequence 38374, A
29	651	27.2	1530	6	US-10-097-559-12	Sequence 12, Appli
30	649.5	27.2	1922	7	US-10-425-114-27875	Sequence 27875, A
31	649.5	27.2	2008	8	US-10-425-115-94743	Sequence 94743, A
32	637.5	26.7	1660	9	US-10-669-962-16	Sequence 16, Appli
33	637	26.7	5822	7	US-10-437-963-3724	Sequence 3724, Ap
34	634	26.5	1615	7	US-10-686-947-259	Sequence 259, App
35	634	26.5	1615	9	US-10-943-507-254	Sequence 254, App
36	633.5	26.5	1610	7	US-10-686-947-197	Sequence 197, App
37	633.5	26.5	1610	9	US-10-686-947-261	Sequence 261, App
38	633.5	26.5	1610	9	US-10-943-507-194	Sequence 194, App
39	633.5	26.5	1610	9	US-10-943-507-256	Sequence 256, App
40	632.5	26.5	1657	7	US-10-686-947-195	Sequence 195, App
41	632.5	26.5	1657	9	US-10-943-507-192	Sequence 192, App
42	631	26.4	1652	7	US-10-686-947-193	Sequence 193, App
43	631	26.4	1652	9	US-10-943-507-190	Sequence 190, App
44	631	26.4	1862	7	US-10-437-963-46212	Sequence 46212, A
45	630.5	26.4	2081	7	US-10-424-599-2618	Sequence 2618, Ap

ALIGNMENTS

RESULT 1
US-10-171-174A-9
; Sequence 9, Application US/10171174A
; Publication No. US20030150012A1
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: Yu, Xiaodan
; TITLE OF INVENTION: A METHOD FOR ALTERING THE ISOFLAVONOID PROFILE IN THE PLANT PART
; FILE REFERENCE: B81452 US NA
; CURRENT APPLICATION NUMBER: US/10/171,174A
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,981
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
US-10-171-174A-9

Alignment Scores:

Pred. No.: 0
Score: 2258.00
Percent Similarity: 86.76%
Best Local Similarity: 86.76%
Query Match: 94.52%
DB: 6
US-09-857-581B-66 (1-521) x US-10-171-174A-9 (1-1756)

Length: 1756
Matches: 452
Conservative: 0
Mismatches: 69
Indels: 0
Gaps: 0

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QY      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db      67 ATGTTCTGGAACTTGCACCTTGAGTTGTTGGTGTAGCTTTGTTCTGCACCTTGCGTCCC 126
QY      21 ThrPro***Ala***SerIysAlaLeuArgHisLeuProAnbProPsePro***Pro 40
Db      127 ACACCAAGTGAATAATCAAAAGCATTCCGCACTCCCAAAACCTCCCAAGCCCAAGCCT 186
QY      41 ArgLeuProPheHisLeuHis***HisLeuLeuLysAspLysLeuLeuHisGlyAla*** 60
Db      187 CGCTTCCCTTCATTGTCACCTTCCTTAAAGATTAACCTTCCTCCACATATGACATC 246
QY      61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
Db      247 ATCGATCTCTCCAAAAGCATGAGCCCTTATCTCTCTCTCCCTCCGCTCCATGCGCAAC 306
QY      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
Db      307 GTGCTTGCCCTCCACCCCTGAGTTGTTCAAGCTCTTCCTCCAAACCCACGAGGCACTTCC 366
QY      101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyTrpAsp*****ValAla 120
Db      367 TTCACACACAGGTTCCAAACCTCTGCCATTAAGACGCTCACTTACGACAACTCTGCGCC 426
QY      121 *****Pro***GlyProTyTrp***PheValArgLysLeuIleMetAsnAspLeu*** 140
Db      427 ATCGTTCCTTCGCGACCTTACTGGAAGTTGTTGAGAGAGCTCATGAAAGCAGCTTCTC 486
QY      141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
Db      487 AACGCACACACCTGCAACAAGCTCAAGGCTTTGAGAGACCCACAGATCCGCAAGTTCCTT 546
QY      161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeu 180
Db      547 AGGGTTATGGCCCAAGAGCGGAGAGGCCACAGAACCCCTTGACCTCCAGAGGCTTCTC 606
QY      181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
Db      607 AATATGACCAACAGCACCATCTCATGATATATGCTCGGCAAGGCTGAGAGATCAAGAGC 666
QY      201 IleAlaArgGluValLeuLysIle***GlyGluTySerLeuThrAspPheIle***Pro 220
Db      667 ATCGCTCGGAGGTTCTTAAGATCTTCGCGGATATACAGCTCACTGACTCATCTGAGCT 726
QY      221 LeuLys***LeuLysValGlyLysTyArgLysArgLysIleAspAspIleLeuAsnLysPhe 240
Db      727 TTGAAGTATCTCAAGGTGGTGAAGATGAAGAGATGATATACATCTTGAACAGTTC 786
QY      241 AspProValIleGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db      787 GACCTGTGCTTAAAGGGTCAATCAGAGAGCGCGTGAGATCGTCAAGAGAGAGAGAGAGC 846
QY      261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
Db      847 GAGAGAGTTGTTAGAGGCGAGGCGAGGCGGCTCTTCCTCGACACTTGTGATTGCTGCT 906
QY      281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db      907 GAGAGACAGACCAATGAGATCAAAATTAACCAAGAGCAAAATCAAGGCGCTGTGTTCGAC 966
QY      301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
Db      967 TTTTCTCTGCAAGGAGCAGATTCCACAGCGGTGGCAACAGAGTGGGCAATTGGGCAAGCTC 1026
QY      321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TySerValIleGlyLys 340
Db      1027 ATCAACAAATCCAGGGGTGTGCAAAAGGCTCGTAGAGAGGTCTACAGTGTGTGGGGA 1086
QY      341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyTrpIleArgAlaIleValLys 360
Db      1087 GATAGACTGCTTACAGAAAGTTGACACTCAAAACCTTCACTTACATTAAGGGCCATTGGAG 1146
QY      361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380

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Db      1147 GAGACATTCGAGATGACACCCACACTCCAGTGTGTAAGAAAGATGCACAGAGGTCT 1206
QY      381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db      1207 GAGATTAAATGGGTATGTATCCAGAGGAGCATTTGTTCTTTCAATTTTGGCAAGTA 1266
QY      401 Gly***Asp***LysTyTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db      1267 GGAAGGAGACCCCAATATCTGGGACAGACCATAGAAATTCGTCGCCAGAGGTTCTTAGA 1326
QY      421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db      1327 ACTGGTGTGGAAGGGAAGCAGGCGCTTGATCTTAGAGGCGCAGACTTCCAACTCCTC 1386
QY      441 ProPheGlySerGlyValArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db      1387 CCATTGGGTGTGGAGAGAGATGTGCTCGTGTGCAATTTGCTAATTCAAGAAATGGCA 1446
QY      461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGln 480
Db      1447 ACACCTTCTGACATCTTATCCAAATGCTTTGACCTGCAAGTCTGAGCCCTCAAGAGCA 1506
QY      481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db      1507 ATATTGAAGGTGATGATGATCCAAAGTTAGCATGGAAGAGAGAGCTGAGCTCAAGTTCA 1566
QY      501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db      1567 AGGGCACAATAGTCTGTTGTGTTCACATTCGAAGATGCGGTGTCATTAACCTCCTT 1626
QY      521 Ser 521
Db      1627 TCT 1629

RESULT 2
US-10-104-706-1
; Sequence 1, Application US/10104706
; Publication No. US20030167507A1
; GENERAL INFORMATION:
; APPLICANT: Odeh, Joan
; APPLICANT: Yu, Xiaodan
; APPLICANT: Lu, Guhua
; APPLICANT: Xu, Hu
; APPLICANT: Ruff, Richard
; TITLE OF INVENTION: Root-Specific, Stimulant Inducible Promoter and its Use
; FILE REFERENCE: B1468 US NA
; CURRENT APPLICATION NUMBER: US/10/104,706
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278379
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-104-706-1

Alignment Scores:
Pred. No.: 0 Length: 1756
Score: 2258.00 Matches: 452
Percent Similarity: 86.76% Conservative: 0
Best Local Similarity: 86.76% Mismatches: 69
Query Match: 94.52% Indels: 0
DB: Gaps: 0

US-09-857-581b-66 (1-521) x US-10-104-706-1 (1-1756)
QY      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db      67 ATGTTCTGGAACTTGCACCTTGAGTTGTTGGTGTAGCTTTGTTCTGCACCTTGCGTCCC 126

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QY 21 ThrPro***Ala***SerIysAlaLeuArgHISLeuProAsnProProSerPro***Pro 40
 DB 127 AACACCAAGGCAAAATCAAAAGACCTTGGCCACCTCCAAACCTCCAAAGCCCAAGCCCT 186
 QY 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisGlyTyrAla*** 60
 DB 187 CGCTCTCCCTTCATTTGGCCACCTTCACTCTTAAAGATTAACCTTCCATATGACATC 246
 QY 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 DB 247 ATCGATCTCTCCAAAAGAGAGCCCTTATTTCTCTCTCTCTCGGCTCATGCTCAAC 306
 QY 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 DB 307 GTCTGTGCTCCACCCCTGAGTTGTTCAAGCTCTTCTCCAAACCAAGAGGCACTTCC 366
 QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 DB 367 TTCACACAAAGTTCCAAACCTCTGCCATPAAGAGCTCCTACGACAACTCTGTGGCC 426
 QY 121 *****Pro***GlyProTyrTTP***PheValArgLysLeuIleMetAsnAspLeu*** 140
 DB 427 ATGTTCCATTCCGACCTTACTGGAAGTTCTGAGAGAGCTCATGAACGACCTTCTC 486
 QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 DB 487 AACGCCAACCCCTCAACAAAGCTCAGGCTTTAGAGACCAACAAAGATCCGCAAGTTCT 546
 QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeu 180
 DB 547 AGGTTATGSCCCAAAGCCGAGAGGCCCAAGAGCCCTTACGTCACGAGAGCTTCTC 606
 QY 181 LysTyr***AsnSerThr***SerMetMet***LeuGlyGluAlaGluIleArgAsp 200
 DB 607 AATATGCAACCAAGACCAATCTCATGATGATGCTCGCAGAGCTGAGGATCAAGAC 666
 QY 201 IleAlaArgLysValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
 DB 667 ATGCTTCGCAAGGTTCTTAAGATCTTGGGCAATACGCTTCACTCATCTTGCCCT 726
 QY 221 LeuLys***LeuLysValGlyLysTyrGlyLysArgIleAspAspIleLeuAsnLysPhe 240
 DB 727 TTGAAGATCTCAAGGTTGAAAGTATGAGAAGAGATGATGATGATGATGATGATGATG 786
 QY 241 AspProValValGluArgValIleLysLysArgArg***IleValAlaArgArg***Asn 260
 DB 787 GACCTGTCTGTTAAAGGTCATCAAGAGGCGCGTGAATCGTCAAGAGAGAGAAAGAC 846
 QY 261 GlyGlu*****GlyGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
 DB 847 GGAAGATGTTGTTGAGGCGAGGCGAGGCGCTCTTCTCCAGACCTTGTGATTGGCT 906
 QY 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
 DB 907 GAGACGACGACCAATGAGATCAAAATTAACAAAGAGCAAAATCAAGGCTTGTGTGCAC 966
 QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTyrPalaleuAlaGluLeu 320
 DB 967 TTTTCTCTGAGGAGACGATTCCACAGCGGTGGCAACAGAGTGGGCACTTGGAGACTC 1026
 QY 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
 DB 1027 ATCAACAAATCCAGAGGAGTGTCAAAAAGCTCTGTAGAGAGTCTACAGTGTGTGGCAA 1086
 QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
 DB 1087 GATGAGACTCGTTGACGAAGTTGACACTCAAAACCTTCTTACATTAGGGCCATTGTGAAG 1146
 QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
 DB 1147 GAGACATTTCGAATGACCAACCACTCCAGGAGGTCAAAAGAGAGTGCAGAGAGAGTGT 1206
 QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTyrGluVal 400

DB 1207 GAGATTAAATGGGTATGATATCCAGAGGAGACATTGCTTTTCAATGTTTGGCAAGTA 1266
 QY 401 Gly***Asp***LysTyrTyrAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 DB 1267 GGAAGGAGACCCCAAAATACGGGAGAGACATCAGAAATCCGTCAGAGAGGTTCTTAGAA 1326
 QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 DB 1327 ACTGTGCTGAAGGGGAGAGAGGAGGCTCTGTATCTTAAGGGCCAGACATTTCAACTCTC 1386
 QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 DB 1387 CCATTGTGCTGGAGAGAGAAATGTCCTGTGTGTCATATTGGCTACTTACAGAAATGGA 1446
 QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
 DB 1447 AACCTTCTTGACATCTTATCCAAATGCTTGAACCTGCAAGTCTGAGGCTCAAGGACAA 1506
 QY 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
 DB 1507 ATATTGAAGGTGATGATGATGCAAGTTAGCATGAGAGAGAGCTGGCTCAAGTTCCA 1566
 QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
 DB 1567 AGGCAACATAGTCTCGTTGTGTTCCATTGCAAGAGATGCGCTTGCATTAACCTCTT 1626
 QY 521 Ser 521
 DB 1627 TCT 1629
 RESULT 3
 US-10-310-154-367
 ; Sequence 367, Application US/10310154
 ; Publication No. US20030233670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; APPLICANT: Chomet, Paul S.
 ; APPLICANT: Adams, Thomas H
 ; APPLICANT: Ruff, Thomas G.
 ; APPLICANT: Agarwal, Ameeta K.
 ; APPLICANT: Ahrens, Jeffrey E.
 ; APPLICANT: Ball, James A.
 ; APPLICANT: Banu, G.
 ; APPLICANT: Bell, Erin
 ; APPLICANT: Boddupalli, Raghava
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Deng, Molian
 ; APPLICANT: Dong, Jintzhuo
 ; APPLICANT: Duff, Stephen M.
 ; APPLICANT: Galligan, Meghan M.
 ; APPLICANT: Hinchey, Brenda S.
 ; APPLICANT: Huang, Shihchieh
 ; APPLICANT: Johnson, G. Richard
 ; APPLICANT: Jung, Vincent
 ; APPLICANT: Kretzmer, Keith A.
 ; APPLICANT: Lacchetti, Lucille B.
 ; APPLICANT: Lai, Chao-Qiang
 ; APPLICANT: Lee, Gary
 ; APPLICANT: Lin, Jie-Yi
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Lu, Bin
 ; APPLICANT: Luedhy, Michael M.
 ; APPLICANT: Lund, Adrian
 ; APPLICANT: Madison, Linda L.
 ; APPLICANT: Malloy, Kathleen A.
 ; APPLICANT: McKel, Christine L.
 ; APPLICANT: Miller, Philip W.
 ; APPLICANT: Padmavathi, Manthikanti
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Start, William G.
 ; APPLICANT: Tennessee, Dan
 ; APPLICANT: Vidya, K. R.

```
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 367
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(1607)
; OTHER INFORMATION:
; US-10-310-154-367

Alignment Scores:
Pred. No.: 0 Length: 1709
Score: 2256.00 Matches: 452
Percent Similarity: 86.76% Conservative: 0
Best Local Similarity: 86.76% Mismatches: 69
Query Match: 94.43% Indels: 0
Gaps: 0
DB: 6

US-09-857-581B-66 (1-521) x US-10-310-154-367 (1-1709)

QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 45 AGTGGCTTGAACCTTCACCTGTTATGTGTTGCTCTGTTGCTGCGCTTGCCTCC 104
QY 21 ThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
DB 105 ACACCCACGCAAAATCAAAAGCACTTCGCCATCTCCCAACCCACCAAGCCCAAGCCT 164
QY 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
DB 165 CGTCTTCCCTTCATAGGACACCTTCATCTTAAAGACAACTTCTCCACTRACGACATC 224
QY 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
DB 225 ATCGACCTCTCCAAAACATGGTCCCTTATCTCTCTACTTGTGGCTCATGCCAACCC 284
QY 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
DB 285 GTTGTGCTCCACACACAGAAATGTTCAAGCTCTTCTCCAAACGACAGGCAACTTCC 344
QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
DB 345 TTCAACACAAAGTTCCAAACCTCAGCCATRAGACGCTCACCTATGATAGCTCAGTGGCC 404
QY 121 *****Pro***GlyProTyrTyr***PheValArgLysLeuIleMetAsnAspLeu*** 140
DB 405 ATGGTTCCTCGGACCTTACTGGAAGTTCTGAGAGAGCTCATGAAACGACTTTC 464
QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
DB 465 AACGCACACACTGTAAACAAAGTTGAGGCTTTGAGGACCCAAACAGATCCGCAAGTCTT 524
QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 180
DB 525 AAGGTTATGGCCCAAGGCGCAGAGGACAGAAAGCCCTTGACCTTGACCGAGAGCTTCTG 584
QY 181 LysTyr***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
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DB 585 AATGAGCAACACAGACACATCTCCATGATGATGCTCGCGGAGGCTGAGAGATCAGAGAC 644
QY 201 IleAlaArgGluValLeuLysIle***GlyGlyTyrSerLeuThrAspPheIle***Pro 220
DB 645 ATCGCTCGGAGGTTCTTAAGATCTTTGGCGAATACAGCTCACTGACTTCACTCGGCCA 704
QY 221 LeuLys***LeuLysValGlyLysTyrGluLysAlaGlyIleAspAspIleLeuAsnLysPhe 240
DB 705 TTGAAGCATCTCAAGGTTGGAAGATRAGAAAGAGATGACAGACATCTTGAACAAGTTC 764
QY 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
DB 765 GACCTGTCTGTGAAGGGTCTCATCAAGAGCCCGTGAATGTGTGAGGAGGAGAAAGAAC 824
QY 261 GlyLys*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
DB 825 GGAAGGTTGTTGAAGGTGAGGTACAGCGGGGTTTCTTGACACTTGTGTAATTCGCT 884
QY 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
DB 885 GAGGATGAGACCATGAGATCAAAATCAACAGACACATCAAGGGTCTTGTTCGAC 944
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGlyLeu 320
DB 945 TTTTCTCGGACAGAACAGACTCCACAGCGGTGCGAACAGAGTGGGCAATTGGCAGAACTC 1004
QY 321 IleAsnAspPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
DB 1005 ATCAACAAATCCTAAGGTGTGGAAGAAAGGCTCGTGAAGAGTTTACAGTGTGTGGAAAG 1064
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
DB 1065 GACAGACTTGTGGAAGAGTGTACACTCAAAACCTTCCTTATATRAGCAATCGTAAG 1124
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
DB 1125 GAGACATTCCTCGCATCACCCGCACTCCAGTGGTCAAAAGAAATGCAACAAAGAGTGT 1184
QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValIleProGlnVal 400
DB 1185 GAGATTATGATATGTGATCCCAAGGAGGATGATTTCTTCAATGTATGGCAAGTA 1244
QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
DB 1245 GGAAGAGACCCCAATACAGGAGACAGACCATCGAGTTCCTGCTGAGAGTTCCTAAG 1304
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
DB 1305 ACAGGGGCTGAAGGGGAGAGCAGGGGCTCTTGATCTTAAGGGGCAACATTTTCAACTTCC 1364
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1365 CCAATTGGGTCTGGAGAGAAATGTGCCCTGAGATCAATCTGCTTACCTCGGAAATGGCA 1424
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
DB 1425 ACACTTCTTGACATCTTATTAAGTCTTCGACTTCGCAAGTCTGGGTCCACAAGAGACAG 1484
QY 481 IleLeuLysGly***AspAlaLysValSerMetCysGluArgAlaGlyLeuThrValPro 500
DB 1485 ATATTGAAGGGGTGTGAGCGCCAAAGTTAGCAAGAGAGAGAGCCGGGCTCTCATCTTCCA 1544
QY 501 ArgAlaHisSerLeuValCysValIleProLeuAlaGlyIleGlyValAlaSerLysLeuLeu 520
DB 1545 AAGGACATATGCTGTGTGTCTCACTTGCAAGATCGGGCTTGACATTAACCTCTT 1604
QY 521 Ser 521
DB 1605 TCT 1607

RESULT 4
US-10-732-923-309
; Sequence 309, Application US/10732923
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SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3
 LENGTH: 1567
 TYPE: DNA
 ORGANISM: Glycine max
 US-10-505-145-3

Alignment Scores:

Prod. No.:	9_65e-317	Length:	1567
Score:	2248.00	Matches:	450
Percent Similarity:	86.56%	Conservative:	1
Best Local Similarity:	86.37%	Mismatches:	70
Query Match:	94.10%	Indels:	0
DB:	9	Gaps:	0

US-09-857-581b-66 (1-521) x US-10-505-145-3 (1-1567)

```

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuAlaGPro 20
      |||::|||
Db      1 ATGGTCTTGAACCTTGACCTGGTTATGTTGGCTCTGTTCTGCACTTGCCTGCC 60
Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
      |||::|||
Db      61 ACACCCACTGCAGAAATCAAAAGCACTTCCGCACTCCCAACCCCAAGCCCAAGCCT 120
Qy      41 ArgLeuProPheHisLeuHis***HisLeuLeuLysAspLysLeuLeuHisTyraAla*** 60
      |||::|||
Db      121 CGTCTTCTTCATAGACACCTTCATCTCTTAAGACAACTTCTCCACTACGCACTC 180
Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer****PheGlySerMetProThr 80
      |||::|||
Db      181 ATGACACTCTCCAAAAAATGATGCTTATCTCTCTACTTGGCTCCATGCCAAC 240
Qy      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln****GluAlaThrSer 100
      |||::|||
Db      241 GTTGTGCTCTCCACACAGCAATGTTCAAGCTCTTCTCCAAAGCAAGGCAACTTCC 300
Qy      101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyraPhe****ValAla 120
      |||::|||
Db      301 TTCAACACAAAGGTTCCAAACCTCCGCCATAGACGCTCCTACCTTATGATGTCAGTGGCA 360
Qy      121 *****Pro***GlyProTyraPhe***PheValArgLysLeuIleMetAsnAspLeu*** 140
      |||::|||
Db      361 ATGTGCTCCTCGGCGCCTACTGGAAGTGTGAGAACTCATCATGAACGACTTCTC 420
Qy      141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
      |||::|||
Db      421 AACGCCACCACTGTAAACAAAGTTGAGGCTTTGAGAACCCCAAGACGCGTAAAGTTCTCT 480
Qy      161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
      |||::|||
Db      481 AGGGTTATAGCCCAAGGCGCAGAGGCACAGAAAGCCCTTGACTTGACCGAGGACTTCTG 540
Qy      181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
      |||::|||
Db      541 AAATGACCAACACACACATCTCATATGATGCTCGGCGAGGCTGAGGATCAGAGAC 600
Qy      201 IleAlaArgGluValLeuLysIle***GlyGluTyraSerLeuThrAspPheIle***Pro 220
      |||::|||
Db      601 ATCCCTCGCAGAGTCTTAAGATCTTGTGGCAATACACCCCTCAGCTTATCTGCGCA 660
Qy      221 LeuLys***LeuLysValGlyLeuTyraGluLysAspGluIleAspAspIleLeuAsnLysPhe 240
      |||::|||
Db      661 TTGAAGCACTTCAGAGTTGAAAGTATGAGAAAGAGATCGACGACATTTGAACAAGTTC 720
Qy      241 AspProValGluValArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
      |||::|||
Db      721 GACCTGTCGTTGAAGAGGTATCAAGAAAGCCGCTGAGATCGTGAAGAGAGAAAGAAC 780
Qy      261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
      |||::|||
Db      781 GGAGAGGTTGTTGAGGAGGTGACGCGGCTTTCTTGACACTTGTGCGAGTTGCT 840
  
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Qy      281 GluAspGluThr***GluIleLysIlePheLys*****Ile***GlyLeuValValAsp 300
      |||::|||
Db      841 GAGAGTGAAGACTATGAGATCAAAATCACCAAGACACACATCAAGGCTTTGTTGAGC 900
Qy      301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuIleGluLeu 320
      |||::|||
Db      901 TTTTCTCGCAGAGAACAGACTCAACAGCGGTGGCAACGAGTGGCATTTGCAAGACTC 960
Qy      321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyraSerValValGlyLys 340
      |||::|||
Db      961 ATCAACAATCTTAAGGTGTGAAAAAGGCTCGTAGAGAGTCTACAGTGTGTGGAAAG 1020
Qy      341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyraIleArgAlaIleValLys 360
      |||::|||
Db      1021 GACAGACTGTGACCAAGTTGACACTCAAAACCTTCTTACCTTACAGCAATCGTGAAG 1080
Qy      361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
      |||::|||
Db      1081 GAGACATTCGCAATGACACCCGCACTCCAGTGTCAAAAGAAAGTGCACAGAAAGTGT 1140
Qy      381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGluVal 400
      |||::|||
Db      1141 GAGATTATGATGATATGATATCCAGAGGAGCATTTCTCTTCAATGATATGCAAGTA 1200
Qy      401 Gly***Asp***LysTyraTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
      |||::|||
Db      1201 GGAAAGAGACCCCAAAATCTGGAGCAGACACATCGAATCTCCGCTCAGAGGTTCTAGAG 1260
Qy      421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
      |||::|||
Db      1261 ACAGGGGCTGAAAGGGAAGAGAGAGGAGGCTCTTGATCTTAAAGGGAACAATTTCACTTCTC 1320
Qy      441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
      |||::|||
Db      1321 CCAATTGGGTCTGGAGAGAAATGTCCTCGAGTCAATCTGCTACTTCCGGAATGGCA 1380
Qy      461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
      |||::|||
Db      1381 ACACCTCTTGCACTCTCTTATTCAGTCTTGCACCTTCAATGCTGGGTCCAAAGACAG 1440
Qy      481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
      |||::|||
Db      1441 ATATTGAAGGCTGTACACCCCAAGTTGATGATGAGAGAGAGACCGGCTCATGTTCCA 1500
Qy      501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
      |||::|||
Db      1501 AGGGCACATAGTCTGTGCTGTTCCTTCACTTGAAGAGATCGGCGTGGCATTAATCTCTT 1560
Qy      521 Ser 521
      |||
Db      1561 TCT 1563
  
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RESULT 7
 US-10-739-930-3497
 Sequence 3497, Application US/10739930
 Publication No. US20040216190A1
 GENERAL INFORMATION:
 APPLICANT: Kovalic, David K.
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
 FILE REFERENCE: 38-21(53577)B
 CURRENT FILING DATE: 2003-12-18
 NUMBER OF SEQ ID NOS: 11088
 SEQ ID NO 3497
 LENGTH: 1974
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER333_17
 US-10-739-930-3497

Alignment Scores:

Pred. No.:	2.04e-299	Length:	1974
Score:	2130.00	Matches:	430
Percent Similarity:	83.11%	Conservative:	3
Best Local Similarity:	82.53%	Mismatches:	78
Query Match:	89.16%	Indels:	10
DB:	8	Gaps:	1

US-09-857-581B-66 (1-521) X US-10-739-930-3497 (1-1974)

OY	1	NestleuLeuGluLeuAlaLeuGlyLeu***ValleuAlaLeuPhe***HisLeuArgPro	20
Db	259	ATGTTGCTGGAACTTGCACCTGGTGTGGTGTAGGCTGGTTCCTGCACCTTCGCTCC	318
OY	21	ThrPro**Ala**SerLeuAlaLeuArgHisLeuProAsnProProSerPro**Pro	40
Db	319	ACACCAACTGCAAAATCAAAAGCACTTGGCACCTCCCAACCTCCAGGCCAAAGCCT	378
OY	41	ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla**	60
Db	379	CGTCCCTCCCTTCATGTGGGACCTTCACCTCTTAAAGATTAACCTTCTCACTAGCACTC	438
OY	61	IleAspLeuSerLysLysHisGlyProleuPheSer*****PheGlySerMetProThr	80
Db	439	ATCAGATCTCTCCAAAAGCATAGGCCCTTATATCTCTCTCTCCGTGGATCATGCAACC	498
OY	81	ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer	100
Db	499	GTCGGGGGGCTCCACCCCTGAGTGTGTCAAGCTCTTCTCCCAACCCAGAGGAACCTTC	558
OY	101	Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla	120
Db	559	TTCAACAACAAGGTTCCAAACCTCTGGCCATTAAGACGCTCACTTACGACAACTGTGGCC	618
OY	121	*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu**	140
Db	619	ATGCTTCATTTGGACCTTACTCGGAAGTTCGGAGAGAACTCATCAATGAAGACCTTCTC	678
OY	141	AsnAlaThrThrValAsn**LeuArgProLeuArgThrGlnGlnIleArgLys**Leu	160
Db	679	AACGCAACACCGACCAACACAGCTCAGGCTTTGAGAGACCAACAGATCCGAACTTCTT	738
OY	161	Arg**MetAlaGln**AlaGluAla**LysProLeuAsp***ThrGluGluLeuLeu	180
Db	739	AGGGTTATGGCCCAAGGACGAGAGGCCCAAGGCCCTTGAAGTCAACGAGAGACTTCTC	798
OY	181	LysTrp**AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp	200
Db	799	AAATGTGACCAACAGCACCATCTCCATGATGATGCTCGCGAGGCTGAGATGATCAGAGAC	858
OY	201	IleAlaIaTgGluValLeuLysIle**GlyGluTyrSerLeuThrAspPheIle**Pro	220
Db	859	ATCGTCCGAGGTTCTTAAATCTTGGCGCAATACAGCCTCACAGCTTATCTGGCCT	918
OY	221	LeuLys**LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe	240
Db	919	TTGAAGTATCTCAAGTGTGGAAGTATGAGAAGAGATGATGATCATCTTGAACAAGTTC	978
OY	241	AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn	260
Db	979	GACCTCGTGTGTTGAAGAGGTCATCAAGAGCGCCGTGAGATCTGACAGAGAGAAGAAC	1038
OY	261	GlyGlu*****GluGlyGlu***SerGlyVal**LeuAspThrLeuLeuGluPheAla	280
Db	1039	GGAGAAAGTTGTGAGGCGGAGGCCCGCGCTTCTCTCGACACTTTCCTTGAATTGCGCT	1098
OY	281	GluAspGluThr**GluIleLysIleThrLys*****Ile***GlyLeuValValAsp	300
Db	1099	GAGGACGAGACCATGAGATCAAAATTACCAAGAGCAAAATCAAGAGGCTTGTTGTGCAC	1158
OY	301	***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu	320
Db	1159	TTTTTCTCTGCGAGGACAGATTTCACACGCGTGGCAACAGATGGCGCACTTGGCAGAGCTC	1218

QY	321	ILEASNANPRO***Valleu*****AlaArgLnuLuu***TyrSerValValAlGlyLys	340
Db	1219	GTGGAGGAGCTTCA-----:-----GCTGTTGGGGCAAA	1248
QY	341	ASP***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys	360
Db	1249	GATGAGACTCGTGGACGAAGTTGACACTCAAACCTTCTTACATTAGGGCATTGTGAAG	1308
QY	361	GLuThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys	380
Db	1309	GAGACATTCCGAATGCACCCACCTCCCAATGGTCAAAAGAAAGTCCACAGAAGAGTGT	1368
QY	381	***IleasnGly***Val1****ProGluGlyValAlau*****PheAsnVal1TrpGlnVal1	400
Db	1369	GAGATTATATGGGATATGGATCCCAAGAGGAGCATTTGTTCTTTTCAATATGTTGGCAAGTA	1428
QY	401	GLY***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu	420
Db	1429	GGAAAGGACCCCAATATCTGGGACAGACCATCAGAA1TTCGTCGCCGAGAGGTTCTTGAA	1488
QY	421	Thr***AlaGluGlyGluVala*****LeuAspLeuArgGly***HisPheGlnLeuLeu	440
Db	1489	ACTGATGCTGAAGGGAGCAAGGAGGCTCTTGATCTTATGGGGCCAGCATTTCCAATCCTCT	1548
QY	441	ProthegLysSerGlyAlaG***MetCysProGlyVal1***LeuAlaThrSerGly***Ala	460
Db	1549	CCATTTTGGGCTCGGAGAGAGAAATGTGCCCTGGCCTCAATTTGGCTACTTCAGGAATGCA	1608
QY	461	ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln	480
Db	1609	ACACTTCTTGCAATCTTATTCCAATGCTTTGACCTGCAAGTGTGGGCTCTCAAGAGCA	1668
QY	481	IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro	500
Db	1669	ATATTGAAAGGTGATGATCCCAAGATTAGATGAAAGAGAGCTGCCCTTCACAGTTCCA	1728
QY	501	ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaIaSerLysLeuLeu	520
Db	1729	AGGCAACATAGTCTCGTTTGTGTTCACCTTGCAAGAGATCGCGCTTGATCTAAACTCCTT	1788
QY	521	Ser 521	
Db	1789	TCT 1791	
RESULT 8			
US-10-411-115-3			
Sequence 3, Application US/10411115			
Publication No. US20040003431A1			
GENERAL INFORMATION:			
APPLICANT: Mizutani, Masako			
APPLICANT: Kasumi, Takaki			
APPLICANT: Ayabe, Shin-ichi			
APPLICANT: Akashi, Tomoyoshi			
TITLE OF INVENTION: Genes Coding for Flavone Synthases			
FILE REFERENCE: 001560-383			
CURRENT APPLICATION NUMBER: US/10/411.115			
CURRENT FILING DATE: 2003-04-11			
PRIOR APPLICATION NUMBER: US/09/672, 785			
PRIOR FILING DATE: 2000-09-29			
PRIOR APPLICATION NUMBER: PCT/JP00/04379			
PRIOR FILING DATE: 2000-01-30			
PRIOR APPLICATION NUMBER: PCT/JP00/00490			
PRIOR FILING DATE: 1999-01-28			
PRIOR APPLICATION NUMBER: JP 11-205229			
PRIOR FILING DATE: 1999-01-19			
PRIOR APPLICATION NUMBER: JP 11-22427			
PRIOR FILING DATE: 1999-01-29			
NUMBER OF SEQ ID NOS: 8			
SOFTWARE: PatentIn version 3.0			
SEQ ID NO 3			
LENGTH: 1730			
TYPE: DNA			
ORGANISM: Torenia hybrida			

FEATURE:
OTHER INFORMATION: Nucleotide sequence encoding a protein having an
OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-115-3

Alignment Scores:

Pred. No.:	2,3e-126	Length:	1730
Score:	944.50	Matches:	198
Percent Similarity:	57.56%	Conservative:	95
Best Local Similarity:	38.90%	Mismatches:	189
Query Match:	39.54%	Indels:	28
DB:	6	Gaps:	8

US-09-857-581b-66 (1-521) x US-10-411-115-3 (1-1730)

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QY 20 ProThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProProserPro*** 39
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 103 CCACCACTTCCTCCCTCCCTCCCTCCGCGA-AGGGAGCACCGCTCCGCGGCTCTTC 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 40 ProArgLeuProPheIleGlyHis**HisLeuLeuIysAspIysLeuLeuHisIYVala 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 162 ---TCCTACCCCAATATTGGCCACCTCCCTCCGCGCAAGA---CTCCACCAACAG 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 60 ***IleAspLeuSerIysIysHisGlyProLeuPheSer****PheGlySerMetPro 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 216 TTCATGAATTTCTACCTCAATACGGCCCATTTGATCCAGCTCAAGCTCGGCTCGATCCG 275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 ThrValValAlaSerThrProGluLeuPheIleLeuGln*****GluAlaThr 99
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 276 TGGCTCTGCGCTCGACGCGCCGACCTCGAGAGATTCTTAAGACGAACGAG--CTC 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 100 SerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrIYrAsp*****Val 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 333 GCGTTCTCTCTCCCAAGCACTCAACGCGCATAGACATCGTCACTACGCTCTCTT 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 Ala*****Pro***GlyProIYrTrp***PheValArgIysLeuIleMetAsnAspLeu 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 393 GCTTCTCTCTCGTACGAGCCCTACTGGAAGTACAAAGAACTGTACTTACCTAGACCTG 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 140 ***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgIys** 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 453 CTCGACGCGAGAACTTCGACACTTCAAGCCCATTTAGGAATCTCGAGGATGCTCTT 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 160 LeuArg***MetAlaGln***AlaGluAla***IysProLeuAsp***ThrGluGluLeu 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 513 CTGACGCTTCTGATGCACAGAGCTTTAAGGCGCAGAGTGTGAATGTGACAGAGACTG 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 LeuIYrTrp***AsnSerThr***SerMetMet***Leu----- 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 573 GTGAGGCTGACGACCAATATGATATCCACATGATGCTGACATTAAGGCTCGGAAGAT 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 193 ---GlyGluAlaGluGluIleArgAspIleAlaArgGluValIleLeuIysIle**GlyGlu 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 633 GAAAGCGATGCTGAGCGCGCGAGAAACAGTGTACCGCGAGGAGCATTTTGGGGAA 692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 TyrSerLeuThrAspPheIle***ProLeuIys***LeuIysValGlyIYrGluIys 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 693 TTCAATGTTACGACATATATATGTTTTCAGAAATATTCATCTGCGAGGGATTAAGAG 752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 232 ArgIleAspAspIleLeuAsnIysPheAspProValValGluArgValIleIysIysArg 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 753 AGGTCAGAGATATTCAGAGAGGATATGATGCTTCTCGAGAGATTAATTAAGATGA 812
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 252 Arg***IleValArgArgArg***AsnGlyGlu*****GluGly-----Glu*** 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 813 GAGAGA-----TCAGAGAGCAAAATCGTATTAAGCATGTGCGGTAAACAATGAGAG 866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 269 SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr**GluIleIys 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 867 GCCAAGATTTCTTGTATATGTTGTTGATGTGATGAGAGAGTGGGAGACAGAGGTCAA 926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 289 IleThrIys*****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSer 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 927 TTCCTAGAGAGCATCTCAAGGCTTTGATTCTGATTTCTTCACGCGCGGTACGACACA 986
QY 309 ThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 987 ACAGCATATGACACGAGAGTGGGCGCATCCGCGAGCTCATCAACACCGCAACCTTTGAAG 1046
QY 329 ***AlaArgGluGlu***TyrSerValValGlyIysAsp***LeuValAspGluValAsp 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1047 AAGGCCCAAGAAATATCCCGATCATCGGAGAACCAACCGGATCTTACAGATCCGAC 1106
QY 349 ThrGlnAsnLeuProTyrIleArgAlaIleValIysGluThrPheArgMetHisProPro 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1107 GCCCAGACCTTACCTTACCTCCAGGCATCATCAAGAGACGTTCCGCTCCACCCACCG 1166
QY 369 LeuProValValIysArgIysCys***GluGluCys***IleAsnGly***Val***Pro 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1167 ATCCGATGCTCTCGGTAAAGTCCACCTCCGATTCGACGCGTCAACCGCTTACAAATCCA 1226
QY 389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysIYrTrpAsp 408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1227 GCCAAGAGCTCTTGTTCGTGAACATATGTCCATCGTCAAACTTAATTACTGGAA 1286
QY 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGluGluAla*** 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1287 AGCCCTATGAGATTCAAGGCCCGACGCGTCTTGGAGAAAGGACCGGAG----- 1334
QY 429 ***LeuAspLeuArgIys***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1335 TCCATGAGAGTCAAAGGCGCAGCACTTGAGCTCTTCCTTTGGAGCGGCGCCAGCGGC 1394
QY 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1395 TGTCTCCGATATGTGCTGTATTAACAAGGTGTCAAGCTCATCTTGTGGACATGTGTGAG 1454
QY 469 CysPheAspLeuGlnValLeuGlyProGlnGlyIleLeuIysGly***AspAlaIys 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1455 TGCTTGAC-----TGAAATTTGCAATGTTTGGGCATTAAT 1493
QY 489 ValSerMetGluGluIuArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1494 GTGACATGACGAGACGAGTGTGATTGACCGCTCCAGAGCGTTCATCTGTTGCGG 1553
QY 509 ProLeuAlaArgIleGlyValAlaSer 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1554 TTGTATCCAGGGTTGACCGGCGACA 1580.

```

RESULT 9

US-10-411-225-3

Sequence 3, Application US/10411225
Publication No. US20040261146A1

GENERAL INFORMATION:

APPLICANT: Mizutani, Masako

APPLICANT: Kasumi, Takaaki

APPLICANT: Ayabe, Shin-ichi

APPLICANT: Akashi, Tomoyoshi

TITLE OF INVENTION: Genes Coding for Flavone Synthases

FILE REFERENCE: 001560-383

CURRENT APPLICATION NUMBER: US/10/411,225

PRIOR FILING DATE: 2003-04-11

PRIOR APPLICATION NUMBER: US/09/672,785

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: PCT/JP00/04379

PRIOR FILING DATE: 2000-01-30

PRIOR APPLICATION NUMBER: PCT/JP00/00490

PRIOR FILING DATE: 1999-01-28

PRIOR APPLICATION NUMBER: JP 11-205229

PRIOR FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: JP 11-22427

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 1730

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; TYPE: DNA
; ORGANISM: Torenia hybrida
; FEATURES:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert Flavanone to Flavone
US-10-411-225-3

Alignment Scores:
Pred. No.:      2,3e-126      Length:      1730
Score:          944.50       Matches:      198
Percent Similarity: 57.56%    Conservative: 95
Best Local Similarity: 38.90%  Mismatches: 189
Query Match:     39.54%      Indels:      28
DB:              8           Gaps:         8

US-09-857-581b-66 (1-521) x US-10-411-225-3 (1-1730)
QY      20  ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProSerPro*** 39
      103  CCAACCACTTCTCTCTCTCTCTCGCGCA-AGGGAGCAACGTCCTCGCGGTCCTC 161
QY      40  ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla 59
      162  ---TCCCTACCCCAATATGGCCACTCCACCTCTCGGCCCAAGA---CTCCACCAACAG 215
QY      60  ***IleAspLeuSerLysHisGlyProLeuPheSer*****PheGlySerMetPro 79
      216  TTCCATGAATTCCTCACTCAATATACGCCCATTTGATCCAGCTCAAGCTCGGCTGATCCG 275
QY      80  ThrValAlaLaserThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThr 99
      276  TGGCGTCGTGGCTCGACGCCCGCAGCTCGCAGAGATTTCTTAAAGCAACAG---CTC 332
QY      100 SerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****Val 119
      333  GCGTCTCTCTCGTCAAGCACTCTACGCCCATAGACATCGTCACTACGACCTGCTCTT 392
QY      120 Ala*****Pro***GlyProTyrTyrPheValArgLysLeuLysLeuLysLeuLysLeu 139
      393  GCTTTCTCTCGTCAAGCACTCTACGCCCATAGACATCGTCACTACGACCTGCTCTT 452
QY      140  ***AsnAlaThrThrValaen***LeuArgProLeuArgThrGlnGlnIleArgLys*** 159
      453  CTCGACGCGAGCAACTCGACACTTTCAGGCCATTTAGAAATCGACGTCAGGCTCTT 512
QY      160  LeuArg***MetLysGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179
      513  CTCGACCTTCTGATGACACAGAGCTTTAAGGCGAGAGTGATGATGACAGACAGAGCTG 572
QY      180  LeuLysTyr***AsnSerThr***SerMetMet***Leu----- 192
      573  GTAGGCTGACGAGCAATGATATCTCCACATGATGCTGAGCATAAGTCTCGGAAGAT 632
QY      193  ---GlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle***GlyGlu 211
      633  GAAGGGGATGCTGAGGCGGAGAACGATATCGCAGGAGACGACATATTTGGGGA 692
QY      212  TyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLys 231
      693  TTCGATGTTACGACATATATGATGTTTGCAGAAATTCGATCTGCGAGGAGTAAGAAC 752
QY      232  ArgIleAspAspIleLeuLeuLysPheAspProValAlaGluArgValIleLysLysArg 251
      753  AGGTCAAGGATATTCAGAGAGGTATGATGCTTTCGACGAAGATATATAGTATAGA 812
QY      252  Arg***IleValArgArgArg***AsnGlyGlu*****GluGly-----Glu*** 268
      813  GAGAGA-----TCGAGAGAGGCAAAATCGGATAGAGATGTCGCGGTACAAATGAGAG 866
QY      269  SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***GluIleLys 288
      867  GCCAAGGATTTTCTTATGATGCTTTCCTTATGATGATGATGAGAGTGGGACACGAGGTC 926

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QY      289  IleThrLys*****Ile***GlyLeuValAlaAsp***PheSerAlaGly***AspSer 308
      927  TTCCTAGAGAGCATCTCAAGGCTTGTGATTCGTGATTTCTTACCGCGCGGTACGACACA 986
QY      309  ThrAla*****ThrGluTyrAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*** 328
      987  ACAGCCATAGCACCGAGTGGGCGCATCGCGAGCTCATCAACACCGCAACGCTTGAAG 1046
QY      329  ***AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAsp 348
      1047  AAGCCCAAGAAATATATCCGATCATCGGAACCAACGCGATGTCTACAGATCCGAC 1106
QY      349  ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
      1107  GCCCCAGACCTACCTCACTCCAGGCATCATCAAGAAACGTTCCGCTCCACCCACCG 1166
QY      369  LeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
      1167  ATCCCGATGCTCTCGGTAAAGTCCACCTCCGATTCGACCGGTCAACCGCTACAAATCCA 1226
QY      389  GluGlyAlaLeu*****PheAsnValTyrGlnValGly***Asp***LysTyrTyrAsp 408
      1227  GCCAAGAGCTCTTGTGTTGTAACATATGTCATGTCGATGTCGAACCTTAATTCGGAA 1286
QY      409  ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
      1287  AGCCCATAGAGTTCAGGCGCCGAGCGGTCTTGGAGAAAGGACGCGAG----- 1334
QY      429  ***LeuAspLeuArgLys***HisPheGlnLeuLeuProPheGlySerGlyArg***Met 448
      1335  TCCATCGACGTCAGAGGCCAGCAGCATTTGAGCTTTCCTTTGGACGCGGCGCAGGCGC 1394
QY      449  CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuLaserLeuIleGln 468
      1395  TGTCCTCGATGTGCTGCGCTATPACAGAGGTGTCAGATCTTGGACCATGTTCCAG 1454
QY      469  CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLys 488
      1455  TGCTTCGAC-----TGGAAATTCGACATGTTCCGCGCAATAT 1493
QY      489  ValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysVal 508
      1494  GTGCACATACCGCAAGCGTGTGATTCGACGCTCCGAGAGCGTTGATGCTGTTTCGCG 1553
QY      509  ProLeuAlaArgIleGlyValAlaLaser 517
      1554  TTGTATCCAGGGGTGACCCGCGCAC 1580

RESULT 10
US-10-411-115-1
; Sequence 1, Application US/10411115
; Publication No. US20040003431A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCES: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411,115
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 1
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-115-1

Alignment Scores:
Pred. No.: 3, 2e-126 Length: 1724
Score: 943.50 Matches: 198
Percent Similarity: 57.314 Conservative: 88
Best Local Similarity: 39.684 Mismatches: 179
Query Match: 39, 498 Indels: 34
DB: Gaps: 9

US-09-857-581b-66 (1-521) x US-10-411-115-1 (1-1724)

QY 33 ProAsnProPsePro***Pro-Arg-----LeuPr 43
DB 87 CCGACCCCTCTTAACCGGACCGCGCAAGACCCCGCGGCCCATTAAGCCTCC 146
QY 43 oPheilegLYHIS***HisLeuLeuLYsAspLYsLeuLeuHISLYrAla***IleAspLe 63
DB 147 CTTAATAGGCACTTACACTCTCTCGGCCAAG---CTCCACACACCTTCCACCAATT 203
QY 63 uSerLYsLYsHISGLYProLeuPheSer*****PheGLYSerMetProThrValValAl 83
DB 204 CTCACACGCTACGCGCGCTCATCCAGCTCTA CTTGCGCTCGCTCCAGCGCTCGCG 263
QY 83 aSerThrProGLuLeuPheLYsLeuPheGLuIn*****GLuAlaThrSerPhe***Th 103
DB 264 TTCACGCGCGCACTCGCGCGCAATTCCTCAAGACCGCACGA---CTGACCTTCTGTC 320
QY 103 rArgPheGLuInThrSerAla***Arg***LeuThrLYrAsp*****ValAla*****Pr 123
DB 321 CCGCAAGCACTCCACCGCCATCGACATCGTCAGTGAAGCTCGTGGCTTCCGCGCC 380
QY 123 o***GLYProLYrTrp***PheValArgLYsLeuIleMetAsnAspLeu***AsnAlaTh 143
DB 381 GTACGGGCGCTACGTGAATTCATCAAGAAATTATGACTTACGAGCTACTGGGTCGCG 440
QY 143 rThrValAsn***LeuArgProLeuArgThrGLuInIleArgLYs***LeuArg***Me 163
DB 441 GAACCTGAGCCATTTCAGCCCATTAAGAGCTTTGAGAGTCAACAGTTTCTTGAGAAATTT 500
QY 163 tAlaGLuIn**AlaGLuAla***LYsProLeuAsp***ThGLuGLuLeuLeuLYrTrp** 183
DB 501 GTACGAGAAAACAGACGAGAAAACAGAGTGTATATGTACAGAGAGCTTGGAAGCTGAC 560
QY 183 *AsnSerThr***SerMetMet***Leu-----GlyGLuAl 195
DB 561 GAGTAATGTGATCATGTAATGTTGGGATCAGGTGTTCCGGGACGGAAGGGGAGGCG 620
QY 195 aGLuGLuIleArgAspIleAlaArgLYsValIleLeuLYrIle***GLYGLuLYrSerLeuTh 215
DB 621 GGAAGTGGCGAGGACGCTGATAGAGAGGAGTACCGAGATATTGGAGGATTTGATGTC 680
QY 215 rAspPheIle***ProLeuLYs***LeuLYsValGLYrLYsGLuLYsArgIleAspAs 235
DB 681 GGAAGATTTGTTGTTGTAAGATTTGATCTCCAGGAGATTGAGGAAGGTGCGAGGA 740
QY 235 pIleLeuAsnLYsPheAspProValValGLuArgValIleLYsLYsArgLYs***IleVa 255
DB 741 TATTAGGAGAGGTATATGCTTTGTTGAGAAAGATTATTTGATAGGAGAGCTTG- 798
QY 255 lArgArgArg***AsnGLYGLuLYs***GLuGLYGLuLYs***SerGLYVal***LeuAspTh 275
DB 799 -AGGTTGAGGGGGGTGTGTGTGAGAGGGGTGAGAGGTGAAGAT---TTTTGGATAT 854
QY 275 rLeuLeuGLuPheAlaGLuAspGLuThr***GLuIleLYsIleThrLYs*****Ile** 295

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DB 855 GTTGTGATGATGATGAGAGTGAAGAAATCGAGGTGAGATTAGAGGAGCATCTCA 914
QY 295 *GLYLeuValValAsp***PheSerAlaGLY***AspSerThrAla*****ThGLuTr 315
DB 915 AGCTTGAATTCGATTTCTTCACTGCGGTGACAGACAAACAGCAATCACAAGCAAG 974
QY 315 pAlaLeuAlaGLuLeuIleAsnAsnPro***ValLeu*****AlaArgGLuGLu***Ty 335
DB 975 GGAATAGAGAGAACTCATTAAGCAATCCAAATTTACTCAAAAAGGCTCAAGAAAGATTGA 1034
QY 335 rSerValValGLYLYsAsp***LeuValAspGLuValAspThrGLuAsnLeuProLYrI 355
DB 1035 CAAGCTAGGATTCACAAAGTTGTGACAGATCCGACGCCCTAATCTTACTTACT 1094
QY 355 eArgAlaIleValLYsGLuThrPheArgMetHisProProLeuProValValLYsArgLY 375
DB 1095 CAACGAGATCAATAAAGAAACGTTCCGTCTCCACCTCCAAATCCCATCTCACTGAAA 1154
QY 375 rCYs***GLuGLuCYs***IleAsnGLY***Val***ProGLuGLYAlaLeu*****Ph 395
DB 1155 ATCAATTTCTGACGTTGTGTCACGCGGTACAGATCCCTGCCMAAACGCTATTGTTGT 1214
QY 395 eLeuValTrpGLuValGLY***Asp***LYsTYrTrpAspArgProSerGLY***ArgPr 415
DB 1215 CAACCTTGTGTCATGGAAGAGATCTTAATCTGGAAGAAATCCGATGAGATCCGAGC 1274
QY 415 oGLuArgPheLeuGLuThr***AlaGLuGLYGLuAla*****LeuAspLeuArgLY** 435
DB 1275 CAGAGGTTCTTCGAGAAAGG-----ACGGGTGATGATGATTAAGGCA 1322
QY 435 *HisPheGLuLeuLeuProPheGLYSerGLYArg***MetCYsProGLYValI***LeuAl 455
DB 1323 GCATTTGAGATTGCTCCGCTTGTGCAAGCGGCGCGGCGGCTGCGCGGATGTTTGA 1382
QY 455 aThrSerGLY***AlaThrLeuLeuAlaSerLeuIleGLuCYsPheAspLeuGLuVal 475
DB 1383 CATGACGAGATTGTTAGTATTAATCGGGCTATGTCAGTGTGATTTGAAACTG-- 1440
QY 475 uGLYProGLuGLuIleLeuLYsGLY***AspAlaLYsValSerMetGLuGLuArgAl 495
DB 1441 ----CCCATGTGTG-----AMGTGCGTGCATGATCCGAGCGGCG 1478
QY 495 aGLYLeuThrValProArgAlaHisSerLeuValCYsValProLeuAlaArgIle 513
DB 1479 CGGTTGACGCGCTCCACGTCGCAATGATTTGTGTCCAATGTGTCCACGAGAT 1533

RESULT 11
US-10-411-225-1
; Sequence 1, Application US/10411225
; Publication No. US20040261146A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411,225
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1724

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/ TYPE: DNA
/ ORGANISM: Antirrhinum majus
/ FEATURE:
/ OTHER INFORMATION: Nucleotide sequence encoding a protein having an
/ OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-225-1

Alignment Scores:
Pred. No.:      3,2e-126      Length:      1724
Score:          943.50      Matches:      198
Percent Similarity: 57.31%      Conservative: 88
Best Local Similarity: 39.68%      Mismatches: 179
Query Match:      39,49%      Indels:      34
DB:              8          Gaps:      9

US-09-857-581b-66 (1-521) x US-10-411-225-1 (1-1724)

QY      33 ProAsnProSerProSerPro***Pro-Arg-----LeuPr 43
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      87 CCAACCTCTCTTAACCCGACCGCCGCAAGACCCGCCGCCGCCATTAGCCCTCC 146

QY      43 oPhelIeglyHis***HisleuleuysAspIysleuHisTyrAla***IleAspIe 63
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      147 CTTAATAGGCGCACTTACACCTCTCGGCGCCAAAG---CTCCACCAACCTTCCACAANT 203

QY      63 uSerIySlySHisGlyProleuPheSer****PheGlySerMetProThrValAlaI 83
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      204 CTCACCAACGCTAGCGCCCGCTCTCAAGCTCTACCTCGCTCCGCCACGCTCGTCCG 263

QY      83 aSerThrProGluLeuPheIysleuPheIeugIn****GluAlaThrSerPhe***Th 103
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      264 TTCACGCGCCGCACTCGCCCGCAATTCCTCAAGACGACGAA---CTGACATTCTGCTC 320

QY      103 rArgPheGInThrSerAla***Arg***LeuThrTyrAsp*****ValAla*****Pr 123
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      321 CCGCAAGACCTCCACCGCATTCGACATCTGTCACGTCAGCTCTGTCGCTTCGCGCC 380

QY      123 o**GlyProTyrTyr***PheValArgIysleuIleMetAsnAspIeu***AsnAlaTh 143
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      381 GTRCGGCGCGTACTGGAATTCATCAAGAAATTGACTTACGAGCTAGCTGCGTCCG 440

QY      143 rThrValAsn***LeuArgProleuArgThrGInIleArgIys***LeuArg***We 163
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      441 GAACCTTGAGCATTCTCCAGCCCATTAAGCTTGAAGCTTCAACAGTTTCTTGAGAAATTT 500

QY      163 rAlaGIn***AlaGluAla***LysProleuAsp***ThGluGluIleuLysTyr** 183
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      501 GTRACGAAACACAGACGACGAAACAGAGTGTAAATGTGACGAGAGCTGTGAAAGCTGAC 560

QY      183 *AsnSerThr***SerMetMet***Leu-----GlyGluAl 195
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      561 GACTAATGTCATCATGTAACATGATGTTGGGAGATCAGGTGCGGACGCAAGGAGAGGC 620

QY      195 aGluGluIleArgAspIleAlaArgGluValIleuLysIle***GlyIleuTyrSerIeuTh 215
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      621 GAGAGTGGCGAGGACGCTGATTAAGGAGGTGACGCAATATTTGGGAGATTGTGATGTC 680

QY      215 rAspPheIle***ProleuLys***LeuLysValGlyLysTyrGluLysArgIleAspAs 235
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      681 GAGAGATTGTTGGTTTGTAAAGATTGATCTGCAAGGGGATTAGGAAGAGGTGCGAGGA 740

QY      235 rIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleVa 255
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      741 TATTAGAGAGAGGATATCATCTTTGTTGGAGAAAGATTATTAGATGAGGAGAGCTTG-- 798

QY      255 lArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspTh 275
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      799 -AGTTGAGAGGGGGGTGTGTGAGAGGGGTGAGAGAGTGAAGAT---TTTTTGATAT 854

QY      275 rIleuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile** 295
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      855 GTTGTGGATGTGATGAGAGTGAAGAAATCGAGGTGAGATTTAAGGAGAGCATCTCAA 914

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QY      295 *GlyLeuValAlaAsp***PheSerAlaGly***AspSerThrAla*****ThGluThr 315
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      915 AGCTTTGATTCTGATTTCTTCACTCGCGGTACAGACACACAGCAATCAACAAGATG 974

QY      315 rAlaLeuAlaGluLeuIleAsnAsnPro***ValIeu*****AlaArgGluGlu***Ty 335
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      975 GGCATATGACGAACATCATTAAGCAATCCAAATATCTCAAAAAAGCTCAAGAAAGATGGA 1034

QY      335 rSerValValGlyLysAsp***LeuValAspGluValAlaAspThrGInAsnIleuProTyrI 355
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1035 CAAGTCATAGATACACAAAGTTGTGCAAGATCCGACGCCCTCACTTGCCTTACCT 1094

QY      355 eArgAlaIleValIysGluThrPheArgMetHisProProleuProValIalIysArgLy 375
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1095 CAACGCAATCATTAAGAAACGTTCCGCTCCACCTCCCAATCCCATGCTCACTAGAAA 1154

QY      375 eCyS***GluGluCyS***IleAsnGly***Val***ProGluGlyAlaIleu*****Ph 395
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1155 ATCAATTTCTGACGTTGTGTGTCACGCGGTACAGATCCTGCGCAAAACGCTATTTGTTGT 1214

QY      395 eAsnValTTPGInValGly***Asp***LysTyrTTPAspArgProSerGlu***ArgPr 415
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1215 CAACCTTGTGTCATAGGAAAGAAATCTTAACCTAGTGAAGAAATCCGATGAGTTCGAC 1274

QY      415 oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspIeuArgGly** 435
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1275 CGAGAGGTTTCTCGAAGAAAGG-----ACCGGCTGATGATGATTAAGAGGCA 1322

QY      435 *HisPheGInLeuLeuProPheGlySerGlyArg***MetCySProGlyVal***LeuAl 455
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1323 GCATTCGAGTTGCTGCGCTGTTGGCAACGCGGCGGCGGCTGCGCGGAGTGTGTTAGG 1382

QY      455 aThrSerGly***AlaThrIleuLeuAlaSerIleuIleGInCySPheAspIeuGInValIe 475
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1383 CATGACGAGGTTGTTAGTATATATCGGGCTATGTCAGTGTTCGATTGGAACGTC-- 1440

QY      475 uGlyProGInGlyGInIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl 495
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1441 ----CCGATGGGTG-----AAGTCGTCGATGATGATGTCGCAATTTGTCACGAGGCG 1478

QY      495 aGlyLeuThrValProArgAlaHisSerIeuValCySValProleuAlaArgIle 513
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1479 CGGGTTGACGGCTCCACGTCGCAATGATTGTGTGTCCAATTTGTCACGAGATT 1533

RESULT 12
US-10-411-115-7
/ Sequence 7, Application US/10411115
/ Publication No. US20040003431A1
/ GENERAL INFORMATION:
/ APPLICANT: Mizutani, Masako
/ APPLICANT: Kasumi, Takaaki
/ APPLICANT: Ayabe, Shin-ichi
/ APPLICANT: Kikuchi, Tomoyoshi
/ TITLE OF INVENTION: Genes Coding for Flavone Synthases
/ FILE REFERENCE: 001560-383
/ CURRENT APPLICATION NUMBER: US/10/411,115
/ CURRENT FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: US/09/672,785
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: PCT/JP00/04379
/ PRIOR FILING DATE: 2000-01-30
/ PRIOR APPLICATION NUMBER: PCT/JP00/00490
/ PRIOR FILING DATE: 1999-01-28
/ PRIOR APPLICATION NUMBER: JP 11-205229
/ PRIOR FILING DATE: 1999-01-19
/ PRIOR APPLICATION NUMBER: JP 11-22427
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 7
/ LENGTH: 1770
/ TYPE: DNA
/ ORGANISM: Perilla frutescens

```

```

; FEATURE: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-115-7

```

Alignment Scores:	
Pred. No.:	5,44e-123
Score:	921.50
Percent Similarity:	57.46%
Best Local Similarity:	38.85%
Query Match:	38.57%
DB:	6
Length:	1770
Matches:	190
Conservative:	91
Mismatches:	183
Indels:	25
Gaps:	8

US-09-857-581B-66 (1-521) X US-10-411-115-7 (1-1770)

Df

OY 33 ProAanProPSePro***ProArGLeuPhePhleIeGIyHse***HisLeuleuLys 52
 |||||
Db 99 CCTTACCCTCCCGGGCGGTTCCT--CTTCCCATCATGGGCCACTTTACACTCCTCCGGG 155

OY 53 AplysLeuUhiEstTyAla***lleaPLeuSerLySylaeGLYPProLeuPheSer 72
 :|||
Db 156 CCGAGA---CTCACCAAAcctTTCCAGCATCTGTCTCCAAGGAAGGACGGGCCTTAATGCAG 212

OY 73 *****PheGLYSerMetProThrValValAlaseThrProGLileuPheLysLeuPhe 92
 :|||:
Db 213 CTCGGCTGGGGTGCCATCCGCTGCCTCATGTGCTGCTCCCGAGAGTCCCAAAGAAATGC 272

OY 93 LeuGlIn*****GluAlathrSerPhe****ThrArgPheGLInthrSerAla***Arg*** 112
 :|||:
Db 273 CTCAACAACACACAGAGCTCGTC--TTCCTCTCCCGAAAACCTCACCGCCATTGATAATC 329

OY 113 LeuThrTYzAsp*****ValAla*****Pro***GlyProTYrTrp**PheValArg 132
 :|||:
Db 330 GTCACTTAGATTCATCCTTCGTCTTCCTCCCTACGGGGCTTACTGAAATCATCAACAA 389

OY 133 LysLeuIlMeMetAsnAspleu***AsnAlathrThValasn**LeuArgProLeuArg 152
 :|||:
Db 390 AAATTATGACCTACACGCTGCTCGGGGCCGAACtgcCCCACTTACGCCCACTACAG 449

OY 153 ThrnglnIlleArgLys***LeuAcg***MetAlglIn**Alagluala**LYSPro 172
 :|||:
Db 450 ACCTCTGAAGTCAAGCTTCTTCTCCAAATTCttatggccaaggtgaattggcgaggagac 509

OY 173 Leuasp***Thrglulinleuleulystrp**AsnserThr**SerMetet***Leu 192
 :|||:
Db 510 TTCAACGTAGTAgAGAGGCTCGGAAGCTGACAGCAAGTCATATGCGATATGATGAGCTG 569

OY 193 -----GlyGluAlgluGlunlleargspillealargGlu 204
 :|||:
Db 570 AGCATACGGTGTTCAGAGACGGAGCGGAGCGGAGCGGAGCGAGTTCGGAG 629

OY 205 ValLeuLyslle***GlyGluYrserLeuThrasPheIlle***ProLeuLys***Leu 224
 :|||:
Db 630 GTCACGACAGATATTTGGAGGTTCGACGTCTCGACATCATATAGCGCTTTTAAAGAACTTC 689

OY 225 LysValGlYrtyrGluLysArgILeaSPAPilLeuaubNlysPheaSPProvalVal 244
 :|||:
Db 690 GATTTCAGAGCTAAGAAAGCGGCTCGAGAGATATCAGAGAGAGATATGATGCTGCTCG 749

OY 245 GluArgValIlleylslySarGaArg***lleValArgArgArg***SaNglyGlu***** 264
 :|||:
Db 750 GAAGAAGATCATKACCGACAGAGAGAG-----CAGAGGGGAGCCACCGCGCGCGTGGC 803

OY 265 GLUGlYGlu**serGlyVal***LeuASPThrLeuengluPhealagluspGluThr 284
 :|||:
Db 804 GGCGGGCGGGAGACCAAGCATTTTCTTGACATGTCTCTCGACATATAGAGAGCGGGAAA 865

OY 285 ***GluIleLysIleThrLys*****Ile***GlyLeuValValJaap***PheSerAla 304
 :|||:
Db 864 GCCGAGATTAATTCACAGGGAGACATCCAAAGCTTGATGTGAGATTTCTTCACCGCC 923

OY 305 Gly***AsperThrAla*****ThrglutPrAlaleuNlagluuelliEasAnPro 32
 :|||:

Db 924 GGCACCGCACGAGCGCGATGTGTGTGAAATGGCGCATAGACGAAGATCAACATACCA 983

Qy 325 **ValLeu*****AlaArgGlu*****TyrSerValValGlyLysAsp**LeuVal 344

Db 984 AATGTGTGAAGAAGCTCAAGAAGATGTCACCAATCGTCGGATTTCGACGAATTCGTG 1043

Qy 345 AspGluValAspThrGlnAsnLeuProTyrPheArgAlaIleValLysGluThrPheArg 364

Db 1044 CAAGAATCCGAGCGCCCAATCTGCGCTTACCTTCAGGCCCTCATCAAGAAACATTCCG 1103

Qy 365 MethisProProLeuProValValLysArgLysCys**GluGluCys**IleAsnGly 384

Db 1104 CTCACACCTCCAAATCCCAATCGTGTGCGAGAAATCGATCTCCGACTGCTCATGACGCGC 1163

Qy 385 **Val***ProGluGluValLeu*****PheAsnValTrpGluValGly**Asp*** 404

Db 1164 TACATGATTCGCGGCAACACGCTCTCTTCGTCAACTCTGTGTCATCGAGGCGGACCT 1223

Qy 405 LysIleTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr**AlaGlu 424

Db 1224 AAAATCTGGAGCTACCCGACGCGCGCTTCACGCGAGAGGTTTCTGGAGAAC----- 1274

Qy 425 GlyGluAla*****LeuAspLeuArgGly**HisPheGlnLeuLeuProPheGlySer 444

Db 1275 ---GAAAGGCGCGCATGATGTTAAAGGCGAGCATTTTGAGCTGTCACTCCGTCGAACG 1331

Qy 445 GlyArg**MetCysProGlyVal**LeuAlaThrSerGly***AlaThrLeuLeuAla 464

Db 1332 GGCAGGAGAGCGCTGCCAGGAGATGTTTACCATTCAGAGGAGGTGCATCAATTAATTCGG 1391

Qy 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484

Db 1392 ACGATGATTCATGCTTGCATTGGAAAGCTG-----CCGACGCG----- 1433

Qy 485 **AspAlaLysValSerMetGluGluIuArgAlaGlyLeuThrValProArgLysHisSer 504

Db 1431 ---TCGGCGCATGTGATATGAGCAGAAAGCGCCAGGCGTCACGCGACCGCGAGACCGAT 1487

Qy 505 LeuValCysValProLeuAlaArgIle 513

Db 1488 TTGTTTGCCGTGTGTGCGCGGAAGTT 1514

RESULT 13

US-10-411-225-7

Sequence 7, Application US/10411225

Publication No. US20040261146A

GENERAL INFORMATION:

GENERAL INFORMATION: Masakko

APPLICANT: Mizutani, Masako

APPLICANT: Kasumi, Takaaki

APPLICANT: Ayabe, Shin-ich

APPLICANT: Akashi, Tomoyoshi

TITLE OF INVENTION:

FILE REFERENCE: 001560-383

FILE REFERENCE: 001580-585
CURRENT APPLICATION NUMBER: IIS/10/411.229

CURRENT APPLICATION NUMBER: US/10/411,223
FILING DATE: 2003-04-11

CURRENT FILING DATE: 2003-04-11

PRIOR APPLICATION NUMBER: US/09/672,785

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: PCT/JP00/04379

PRIOR FILING DATE: 2000-01-30

PRIOR APPLICATION NUMBER: PCT/JP00/00490

PRIOR FILING DATE: 1999-01-28

PRIOR FILING DATE: 1999-01-26
PRIOR ADDITION NUMBER: JP 11-205229

PRIOR APPLICATION NUMBER: JP 11-205229

PRIOR FILING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: JP 11-22427

PRIOR FILING DATE: 1999-01-29 ;

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

COLLATERAL: ACCORDANCE WITH THE
SEO ID NO 7

; SEX ID NO ;
; LENGTH: 1770

! LENGTH: 1770
===== DNA

OTHER INFORMATION: Nucleotide sequence encoding a protein having an

OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-225-7

US-10-411-225-7

Alignment Scores:

Pred. No.: 5.44e-123

Score: _____

Percent Similarity

Best Local Similarity

Query Match:

Length: 1770
Matches: 190

Conservative: 91

Mismatches: 183

Indels:	25
Misscalls:	103

Indels:	25
Gaps:	8

Gaps: 8

US-09-857-581B-66 (1-521) X US-10-411-225-7 (1-1770)

QY	33	ProAnpProPioSerPro***ProAglLeuPioPheIIsgLYhiS***HisLeuLeuLys	52
Db	99	CCCTACCTCCCGGGCGGTTCCT---CTTCCATCATGGCGCACTTAAACCTCTCGGG	155
QY	53	AspLysLeuLeuHisTyrAla***IIeaPLeuSerLysLysHISGLYPProLeuPheSer	72
Db	156	CCGAGA---CTCCACCAAAACCTTCCACGATCTGTCCCAACGGTAACGGCCCTTAATGCAG	212
QY	73	*****PheGLySerMetProThrValIAlaSerThProGluLeuPheLysLeuPhe	92
Db	213	CTCCGCCCTCGGGTTCATCCGCTGCGATTCCTGCTCCTCGCGGAGCTCGCCAAAGAAATGC	272
QY	93	LeuGln****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***	112
Db	273	CTCAAGACACACAGAGCTGC---TTCTCCTCCCGAAACATCCACCGCCATTGATATC	329
QY	113	LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheValArg	132
Db	330	GTCACCTACGATTTCATCCTTCGCTTCTCTCCTACGAGGCTTACTGAAATTCATCAAG	389
QY	133	LysLeuIIeMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArg	152
Db	390	AAATTATGACCTACGAGCTGCGGGCCGAAATCTGCGCACCTTGACCCCATCAGG	449
QY	153	ThrGlnGlnIIeArgLys***LeuArg***MetAlGln***AlaGluAla***LysPro	172
Db	450	ACTCTCGAAGTCAGACTTCTCTCCAAATCTTATACGCAAGGTGATTCGGGGAGAGC	509
QY	173	LeuAsp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu	192
Db	510	TTCAACGTAAGTACGAGAGCTCGTAAGACGTACAGACAGACATCATGCTATGATGCTG	565
QY	193	-----GlyGluAlaGluGluIIeArgAspIIeAlaArgGlu	204
Db	570	AGCATACGAGTGTTCAGACGAGAGTCGAGAGCGGAGCGGACGAGACGATTCGGAG	629
QY	205	ValLeuLysIIe***GlyGluTyrSerLeuThrAspPheIIe***ProLeuLys***Leu	224
Db	630	GTCACGCGAGATTTTGGGAGTTTCGACGCTCCGCAATCATTAAGCTTTGTAAGAACTTC	669
QY	225	LysValGlyLysTyrGluLysArgIIeAspAspIIeLeuAsnLysPheAspProVal	244
Db	690	GATTTCCAAAGATATAAGAAAGCGGTCCGAGAGATTCAGAGAGATATGATGCTGCTG	749
QY	245	GluArgValIIeLysLysArgArg***IIeValArgArgArg***AsnGlyGlu*****	264
Db	750	CAGAGATCATCACCGACAGACAGAGA---CAGAGCGGACCCACGCGCGCGTGGC	803
QY	265	GluGlyGlu***SerGlyVal***LeuAspThrLeuGluGluPheAlaGluAspGluThr	284
Db	804	GGCGGGGGGGAAGCCAGAAATTTTCTTGAAATGTTCTCTGCACATATGAGAGCGGAAA	863
QY	285	**GluIIeLysIIeThrLys*****IIe***GlyLeuValLysp***PheSerAla	304
Db	864	GCCGAAGTTAAATTCACGAGGAGCATCTCAAGCTTTGATGTTCTGATTTCTTACACGCC	923
QY	305	Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIIeAsnAspPro	324
Db	924	GGCACCAGACAGACGGCGATGCTGTGTGAATGGCGATATCAAGAGATCAACAAATCCA	983

US-09-857-581B-66 (1-521) x US-10-424-599-6882 (1-1841)

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OY 325 ***ValLeu*****AlaaGgLUglU**TySerVaValGlyLysAsp***LeuVal 344
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 984 AATGTGTTGAAGAAAGCTCAAGAAAGATTGGCAACACTCTGTGGATTTCACAGAAATCTG 1043

OY 345 AspGluValAspThrGlnAsnLeuProTyrTleArgAlaIleValLysGluThrPheArg 364
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1044 CAAGAAATCCACAGCGCCCAAACTGTGCTTACCTTCACAGCCCTTCATCAAGAAACATTCGCG 1103

OY 365 MetHisProProLeuPcovaIleValArgLysCys***GluLysCys***IleasnGly 384
      ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1104 CTCACCCCTCCAAATCCCAATGCTGGGAGAGAAATTCGATCTCCGACTGCTCATCGAGGC 1163

OY 385 ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnValGly***Asp*** 404
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1164 TACATGATTCGGCGCAACAGCTGCTCTTGTGTCACTCTGTGTCAATGGGCGGAACCT 1223

OY 405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1224 AAAATCTGGGACTCCCGACGGCGCTTCACGCCGAGAGGTTTCTGGGAAG----- 1274

OY 425 GlyValuAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
      ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1275 ---GAAAAGCCCGCCATCGATGTTAAAGGACAGCATTTAGCTGCTTACCGTTGGAACG 1331

OY 445 GlyArg***MetCysProGlyVal**LeuAlaThrSerGly***AlaThrLeuAla 464
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1332 GGCAGGAGAGGCGTCCGAGGGATGCTTTTGGCATTCAGAGGNGTCATCATATATGGG 1391

OY 465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1392 ACGATGATTCATAGTCTTCGATTGGAGCTG-----CCGACGCG----- 1430

OY 485 ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1431 ---TCCGGCCATGTTGATATGGCAGAACGCGCCAGGGCTCACGGCACCCGAGAGCCGAT 1487

OY 505 LeuValCysValProLeuAlaArgIle 513
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1488 TTGTTTGGCGGTGTGTGTGCGCGAGT 1514

RESULT 14
US-10-424-599-6882
; Sequence 6882, Application US/10424599
; Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongmei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 6882
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106222C.1
US-10-424-599-6882

Alignment Scores:
Pred. No.: 1,13e-122 Length: 1841
Score: 919.50 Matches: 198
Percent Similarity: 57.14% Conservative: 86
Best Local Similarity: 39.84% Mismatches: 184
Query Match: 38.49% Indels: 29
DB: 7 Gaps: 9

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QY      29 LeuArgHisLeuProAsnProSerPro***ProArg---LeuProPheIleGlyHis 47
      139 CTCGCCCAAGAGCTCGCGGTCCA---CCGGGCCCAAGGCTCCTCCCATCATCGCCAC 195
QY      48 ***HisLeuLeuLeuAspLeuLeuHisLeuLeuAla***IleAspLeuSerLeuHis 67
      196 CTCATCATCATC---TCCGCCCTGCCTCACCACTCTTCCACGCGCTCTCCACGCGCTAC 252
QY      68 GlyProLeuPheSer*****PheGlySerMetProThrValValAlaSerThrProGlu 87
      253 GGCCTCCGCGCTGCAAGCTTCTCTCGGCTCGCTCCGCGCTGCTGCTTCTGTCGCCGAA 312
QY      88 LeuPheLeuLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThr 107
      313 CTCGCCAAGAGAGTCTCTGAAAGCAAGCAGAG---CCACGCTTCCGAACCGGCTTCGAGT 369
QY      108 SerAla***Arg***LeuThrTyr---Asp*****ValAla*****Pro***GlyPro 126
      370 GCAGCGGTTACACCACTGCTCTATGGGTCACAGGGGTTCTCTCGCGCTTCAGCAAGC 429
QY      127 TyrTrp***PheValArgLeuLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn 146
      430 TACTGAGGTTCTTGAAGAGATTTCATGTCGAGCTTCTCGGTGCGCCGACCTTCGAC 489
QY      147 ***LeuArgProLeuArgThrGlnGlnIleArgHis***LeuArg***MetAlaGln** 166
      490 CAGTTCGCGACCTTGAAGGAGCAAGAACTTGAAGTTTCGGCGCTGAGGGCGGAA 549
QY      167 AlaGluAla***IysProLeuAsp***ThrGluGluLeuLeuIle***AsnSerThr 186
      550 GGGAGAGCGCATGAGCGCTGATGTTAGTGGGAGTTGATGACTTTCACCAAGTGA 609
QY      187 ***SerMetLeu***Leu-----GlyGluAlaGluGluIle 198
      610 ATATCGAGATGTTTGAAGTTCGAACATGTTGCGAGCGCATGTTGCGTGAAGCAGCTG 669
QY      199 ArgAspIleAlaArgGluValIleLeuIle***GlyGluTyrSerLeuThrAspPheIle 218
      670 AGGAAGATGTTGGCGGACACTGCTGAGCTGGCGGGAAGTTCACTTGGGGATTTTGTG 729
QY      219 ***ProLeuIys***LeuIysValGlyLeuTyrGlyIysArgIleAspAspIleLeuAsn 238
      730 TGGTTGTTAAGGGGTTGATTTGATGCGATGCGATAAGAGGCTTGTGGGATTTTGGAG 789
QY      239 LysPheAspProValIleGluArgValIleLeuIysArgArg***IleValArgArgArg 258
      790 AGGTTTATGTCATGATGAGCAGGGTATTAAGGAGCATGAGAGAGAGGAGAGAGAGG 849
QY      259 ***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGlu 278
      850 AAG-----GAAAGAGGGAGAGGGAGAGAGATTAAGGATTTGCTAGATTTTGTGAA 903
QY      279 PheAlaGluAspGluThr***GluIleLeuIleThrIys*****Ile***GlyLeuVal 298
      904 ATTCATCAAGATGAGAGAGGAGATCAAGTTATCTAGAGAGATTCAGAGGCTTTCATC 963
QY      299 ValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAla 318
      964 TTGACACTATATATATGAGCAAGAACACACATCAGCTATATACCATGAGATGGGCTTGA 1023
QY      319 GluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValVal 338
      1024 GAGTTATCAACACATCATCTGATGAGAGAGAGAGAGAGAGAGATTCATGATGACA 1083
QY      339 GlyIysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIle 358
      1084 GGGAAACAAAGAGCTTATCAAGATTCAGATCTTCCCAACCTTCATACCTTCAGAGCCTTA 1143
QY      359 ValIysGluThrPheArgMetHisProProLeuProValIleValIysArgIysCys***Glu 378
      1144 GTCAAGAGAACCTTAAGATTCACCTTACAGGCGCATCTGTAAGAGAGAAATCATCAGAA 1203
QY      379 GluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrp 398

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Db      1204 AACTGCATATGATGCGCTATGACATTCAGAAAGTCTTATGTTTATCTGTG 1263
QY      399 GlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPhe 418
      1264 TCTATGGAGAGGAGCCCAAAATTTGGAGAGACCTCTTGAATCAAGCAGAGAGGTTT 1323
QY      419 LeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGln 438
      1324 ATGAC-----AATATATGAGACAAACAAATGATGATGAGGAGAGAGATTTCCAG 1374
QY      439 LeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly 458
      1375 CTATTCCTATTTGGAGCTGGAGAGAGTGTGTGCTGCTGATCATCTTGCATTCAGACT 1434
QY      459 ***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGln 478
      1435 GTGCCCTACTAAGCTTCTGCTATGATTCATATGTTGAATTTAGGGTT----- 1482
QY      479 GlyGlnIleLeuLeuGly***AspAlaIysValSerMetGluGluArgAlaGlyLeuThr 498
      1483 -----GATGGAGCTGTATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1521
QY      499 ValProArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyVal 515
      1522 CTTCCTAAGGACATCTTGTGATTTGTGTCTGTCCAGCATGAACTT 1572

RESULT 15
US-10-424-599-78567
; Sequence 78567, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 285684
; SEQ ID NO 78567
; LENGTH: 3328
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41962C.1
; US-10-424-599-78567

Alignment Scores:
Pred. No.: 3,74e-116 Length: 3328
Score: 877.50 Matches: 188
Percent Similarity: 57.03% Mismatches: 92
Best Local Similarity: 38.29% Indels: 28
Query Match: 36.73% Gaps: 8
DB: 7

US-09-857-581b-66 (1-521) x US-10-424-599-78567 (1-3328)
QY      35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLeuAspLys 54
      176 CCAACCAAGTCCA---AAGGCCCTTCCATATATGGCCACCTTCACCTTGTG---TCCCA 229
QY      55 LeuLeuHisTyrAla***IleAspLeuSerLeuIysHisGlyProLeuPheSer***** 74
      230 ATTCCCAACCAAGATTTTATCAAGCTTCAACCCGACGAGACCATCATGCAACTTTTC 289
QY      75 PheGlySerMetProThrValIleAlaSerThrProGluLeuPheLeuGln 94
      290 CTGGCTCAGTCCCTGTGTGTGTGCTTCCACCGCAAGAGCGCCCAAGAGAGTTCTTAAA 349
QY      95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114

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Db      350 ACCCGAATAATCACTTCCAAACCGCCCGCCAAACCTCCCTTAAGGCTTAAGC 409
QY      115 TyrAsp*****ValAla*****Pro**GlyProTyrTrp**PheVal 131
Db      410 TAGAATATCCCAAGACTTCTCTTTTCGGTTTGCACTTCGACCTTACCTGAGAGTTCAG 469
QY      132 ArgGlyLeuLeuMetAsnAspLeu***AsnAlaThrThrValAsn**LeuArgProLeu 151
Db      470 AAGAAATCTGCAATGTCGAGCTTCTCAGCGCCGAATGATGAGCAAGTTCCTTCCCGTG 529
QY      152 ArgThr-GlnGlnIleArgLys**LeuArg**MetAlaGln**AlaGlnAla**Lys 171
Db      530 AGGCTGACCAAGACCAAGACCAAGATTCACAGCCCGCGTTCGAAAGAGATGCCCGGCA 589
QY      171 sProLeuAsp**ThrGlnGlnLeuLeuLysTrp**AsnSerThr**SerMetCec** 191
Db      590 GGCCTGTGATTCGAGACGAGCTCATGACACTCTCCACACATCGTATCCAGAAATGAC 649
QY      191 *Leu-----GlyGlnIleGlnIleArgAspIleAlaIar 203
Db      650 GCTGAGTCAAGAGACTTCTGAGAACAGAACAGGCTGAGAGATGAGAGAGCTCGTGC 709
QY      203 gGluValIleuLysIle**GlyGlnTyrSerLeuThrAspPheIle**ProLeuLys** 223
Db      710 GAATATCGGGAGACTCATGCGGAAGTTCACAGTTTCGGAATTCATTTCGTAACCTGAAGCC 769
QY      223 *LeuLysValGlyLysTyrGlnLysArgIleAspAspIleLeuAsnLysPheAspProVa 243
Db      770 TTTCGATTGACGAGGTTCAACCAAGAAATCAAGGAGACTCGGGACAGGTTTGACGTTGT 829
QY      243 lValGlnArgValIleLysLysArgArg***IleValArgArgArg**AsnGlyGln** 263
Db      830 GGTGACGGAATATATAAGCAGCTCAAGAG-----GAAAGAGAGAGAGAGAGAGAAC 883
QY      263 ***GlnGlyGln**SerGlyVal**LeuAspThrLeuLeuGlnPheAlaGlnAspGI 283
Db      884 GGGCAGACAGCAGCGAGTTTAAGGATATGCTGATGTTTATTTGACATAGCGAAGATGA 943
QY      283 uThr***GlnIleLysIleThrLys*****Ile**GlyLeuValValAsp**PheSe 303
Db      944 CAGTTCTGAATCAATTAACCAAGAAACATTAAGGCTTCATCATGATATATTTGT 1003
QY      303 rAlaGly**AspSerThrAla*****ThrGlnTrpAlaLeuAlaGlnLeuIleAsnAs 323
Db      1004 TGCCTGGAGACTGACACGTCAGCTGCACATGAGAAATGGCTATGGCCAGAGTTAATCAACA 1063
QY      323 nPro***ValIleu*****AlaArgGlnGlu**TyrSerValValGlyLysAsp**Le 343
Db      1064 TCCATATGTTGTTGAGAGAGCAAGGCAAGGATATAGATCGCGTGTGAGAAAAGTAGAAT 1123
QY      343 uValAspGlnValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGlnThrPh 363
Db      1124 GGTAGAGAGATCAGATATTCACCACTTCTTACTTCAGACCATTTGTTAGAGAAACACT 1183
QY      363 eArgMetHisProProLeuProValValLysArgLysCys**GlnGlnCys**IleAs 383
Db      1184 TAGGCTTCACCCAGGTGCTCATTTGTTAGAGAAATCATCAAAAAGTCCGGTGGTTTG 1243
QY      383 nGly***Val**ProGlnGlnValAlaLeu*****PheAsnValTrpGlnValGly**As 403
Db      1244 TGGGTATGATATTCAGCAAGAACTGCATATTTGTCAATGTTTGGGCTATTTGGTAGGGA 1303
QY      403 p***LysTyrTrpAspArgProSerGln**ArgProGlnArgPheLeuGlnThr**Al 423
Db      1304 TCCCAATCACTGGAGAGAACTTTTGAGTTTAGGCCAGAGAGGTTTATCAGA----- 1355
QY      423 aGlnGlyGlnAla*****LeuAspLeuArgGly**HisPheGlnLeuLeuProPheGI 443
Db      1356 -GATGGGCAA--AATCAATTGATGTTAGGGGCAACATTAATCATTTTATTCATTGCG 1411
QY      443 ySerGlyArg**MetCysProGlyVal**LeuAlaThrSerGly**AlaThrLeuLe 463

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Db      1412 GAGTGAGAAAGAACGTCGCTGTGCTTCTTACGCTGGCAGGTTGTCCTGTGAATCT 1471
QY      463 uAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlnIleLeuLys 483
Db      1472 GGTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1520
QY      483 sGly**AspAlaLysValSerMetGlnGlnLysArgAlaGlyLeuThrValProArgAlaH 503
Db      1521 -----AAGTGGACATGGAAGAAAGTCTGGCATCACTCTCCAGAGGCTTA 1567
QY      503 sSerLeuValCysValProLeuAlaArgIle 513
Db      1568 CCCCATATTTGTTGTCCTGTTCCAAAGGATT 1598

```

Search completed: December 22, 2005, 02:36:31
Job time : 1016 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2005, 00:03:14 | Search time 44 Seconds
(without alignments)
84.451 Million cell updates/sec

Title: US-09-857-581B-66
Perfect score: 2389
Sequence: 1 MLEFALGLXVLAFLXHLR.....ASHLVCPVLRIGVASKLLS 521

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 53982 segs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA New:
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB pep.*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB pep.*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB pep.*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB pep.*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB pep.*
6: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB pep.*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB pep.*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	398	16.7	524	US-10-667-295-207	Sequence 207, App
2	398	16.7	531	US-10-667-295-206	Sequence 206, App
3	398	16.7	540	US-10-667-295-140	Sequence 205, App
4	387.5	16.2	506	US-10-667-295-140	Sequence 140, App
5	387.5	16.2	526	US-10-667-295-139	Sequence 139, App
6	381.5	16.0	505	US-10-667-295-82	Sequence 82, App1
7	381.5	16.0	534	US-10-667-295-81	Sequence 81, App1
8	327	13.3	434	US-10-667-295-141	Sequence 141, App
9	317	13.3	433	US-10-667-295-83	Sequence 83, App1
10	240.5	10.1	502	US-10-821-234-1554	Sequence 1554, App
11	226.5	9.5	504	US-10-131-826A-64	Sequence 64, App1
12	191	8.0	524	US-11-102-240-54	Sequence 54, App1
13	190	8.0	524	US-11-000-463-877	Sequence 877, App
14	190	8.0	524	US-11-000-463-878	Sequence 878, App
15	190	8.0	524	US-11-000-463-879	Sequence 879, App
16	187	7.8	546	US-11-000-463-805	Sequence 405, App
17	186.5	7.8	490	US-10-507-106-2	Sequence 2, App1
18	183	7.7	568	US-11-000-463-406	Sequence 406, App1
19	181	7.6	468	US-10-957-569-28	Sequence 28, App1
20	181	7.6	520	US-10-995-561-598	Sequence 598, App
21	179.5	7.5	520	US-10-667-295-250	Sequence 250, App
22	178.5	7.5	520	US-10-995-561-597	Sequence 597, App
23	178.5	7.5	520	US-10-995-561-599	Sequence 599, App
24	175.5	7.3	429	US-11-000-463-407	Sequence 407, App
25	161.5	6.8	503	US-10-821-234-1527	Sequence 1527, App

26	158	6.6	524	US-10-507-106-4	Sequence 4, App1
27	157	6.6	509	US-10-131-826A-108	Sequence 108, App
28	155	6.5	498	US-10-667-295-249	Sequence 249, App
29	150.5	6.3	347	US-11-186-284-226	Sequence 226, App
30	142.5	6.0	521	US-10-821-234-1546	Sequence 1546, App
31	103.5	4.3	147	US-10-667-295-19	Sequence 19, App1
32	103.5	4.3	404	US-10-497-135-3	Sequence 3, App1
33	100.5	4.2	404	US-10-497-135-4	Sequence 4, App1
34	97.5	4.1	406	US-11-075-185-23	Sequence 23, App1
35	84.5	3.5	386	US-10-497-135-20	Sequence 20, App1
36	83	3.5	388	US-10-497-135-19	Sequence 19, App1
37	78	3.0	397	US-11-143-980-51	Sequence 51, App1
38	71.5	3.0	1976	US-11-069-834-54	Sequence 54, App1
39	69.5	2.9	638	US-10-488-517-260	Sequence 260, App
40	69.5	2.9	1652	US-10-995-561-663	Sequence 663, App
41	69.5	2.9	1938	US-10-995-561-661	Sequence 661, App
42	69.5	2.9	1938	US-10-995-561-662	Sequence 662, App
43	69.5	2.9	1954	US-10-995-561-660	Sequence 660, App
44	69.5	2.9	1972	US-10-995-561-664	Sequence 664, App
45	69.5	2.9	1972	US-10-995-561-666	Sequence 666, App

ALIGNMENTS

RESULT 1
US-10-667-295-207
; Sequence 207, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(524)
; OTHER INFORMATION: Ceres Seq. ID no. 12450443
US-10-667-295-207

Query Match	16.7%	Score 398	DB 6	Length 524
Best Local Similarity	27.1%	Pred. No. 2e-37		
Matches 132	Conservative 77	Mismatches 220	Indels 58	Gaps 18
QY	35	PSPPKRLPFIQGHXHLKRLHYXIIDSKKHGPFSSXFGSMPTVVASTPELFTLFIQ	94	
DB	52	PPGP-PAVVFPGWGLQVGNLHRRFLARISARGPVRLGLGRNLVVSDFPLAEVTH	110	
QY	95	XXEATSFYTRFQSAKRLTYDXVA-----XXPYGYMXFVRKLIMNDLNATTVNXL	148	
DB	111	-TGVFFGSR-----PRNVFDLTNGADMTVEFGDHRRRRRVWTLPFFARVVOQ	164	
QY	149	RPLRTOQIRKRLKXMAOKXBAKKPLDYTEEL-LKWNSTXSMWKLGEABIRP-----	200	
DB	165	RGWWEAEMLDAVDSVSAQRAAGLVRRRLQMLYINWGMFDPARFGSVDDPMVEAT	224	
QY	201	---IAEVLKIXEYSLTFIXLKLKVGKYEKRIDI---LNKEDPVERIKRRX	253	
DB	225	RNSERSRLAQSFVIVGDTIPVLRPLKQ-YLRCKDLQARLAFN---SNYVERRK	280	
QY	254	IVRRRNKGEKXEGXGVXLDLLEFADETEYIKITKXXIXGLVVDXPSAGXSTPAXXT	313	
DB	281	VM-----DAPDDKQKLK-CAIDHVLQ-AEKSG---ETTPENVIVYVENINVAIETLMSI	331	

[illegible]

```

RESULT 2
US-10-667-295-206
/ Sequence 206, Application US/10667295
/ Publication No. US2005025793A1
/ GENERAL INFORMATION:
/ APPLICANT: Mascia, Peter
/ TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
/ FILE REFERENCE: 11696-047001
/ CURRENT APPLICATION NUMBER: US/10/667,295
/ CURRENT FILING DATE: 2003-09-17
/ PRIOR APPLICATION NUMBER: 05/60/411,823
/ PRIOR FILING DATE: 2002-09-17
/ NUMBER OF SEQ ID NOS: 263
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 206
/ LENGTH: 531
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (1...(531))
/ OTHER INFORMATION: Ceres Seq. ID no. 12450442
US-10-667-295-206

```

Query Match	16.7%;	Score 398;	DB 6;	Length 531;
Best Local Similarity	27.1%;	Pred. No. 2.1e-37;		
Matches 132; Conservative	77;	Mismatches 220;	Indels 58;	Gaps 18;

```

Oy 35 PPSKPRJLPEFIHXLHKLKCLHXYAIDIDSXKHGJPFSSXFGSMPTVASTPELFTLFLQ 94
Db 59 PPGP-PAWVFGNMLOVGVNDLNHRFLARLSARYGVRFLRLGVRNLVVSDPLATEVLH 117
Oy 95 XXEATSFYTRPQTSAXRKLTYDXVA-----XXPYGYMXFVRKLIIMDLXNATTVNXL 148
Db 118 -TQGVFSGR-----PRNVFPDIPTANGADMVFTEXGDHMRRRRRWMLTLEFFARVVQY 171
Oy 149 RPLRTQOIRKXILRXMAQXAAXKPLDXTEEL-LKMXNSTXSMXLCGEABIRD----- 200
Db 172 RGMFEAEMDAASDVASAQRAAGLVRRRLQIMLTNINMGMFDFARFGSVDDPMFEAT 231
Oy 201 ---IAREVLKIXGEVSLTDFIKPLKXLRKGYEKRIDL----LNFDPVBEVIKKRX 253
Db 232 RENSERSRLAOSFDVNYGDFIPVLRFLRG-YIARCKLOARLAFEN---SNVYKRRK 287
Oy 254 IYRRRXNGEXXGEGSGVXLDTLLEBAEDBEXIKLTKXXIXGLVVDPSAGDSFAXXT 313
Db 288 VM----DAPGDXKLR-CAIDHYLO-AEKS--EITPENVIYIVENINVALEITLMSI 338
Oy 314 EWALAEILNPPVYLXXAREEXYSVVGKDLVDEVDQNLPLYIAIYKETFRRMPPLP-VV 372
Db 339 EWALAEVNVHPRVQRKVRDEIKAVVADHBPITESTIHLRPLYOAVIKETIRLHSLPIPLV 398
Oy 373 KRKCEBECKINGXVPEGALXXFNWVOVGDXKKYMDRPSXEKPERFLUTYABGEAXXLDL 432
Db 399 PHMNLIEALGCTTIPKSGKVVUNWAMMLNPNELPMKPEEFRRERF-----GEKSVDA 453

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QY      433  R---GXHOLLPFSGGGRXMCCEVNLATSGXATLALSLIQCFDLYGVGPGQILKGDARY 489
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      454  TVGCKNDRFRLPFRVGRGRSCGPIILALPLIALIVGKLVKSPFM---VPPFQV-----EKL 505
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      490  SMEERAG 496
          :  |||  |
Db      506  DYSEKGG 512
          :  |||  |

```

```

RESULT 3
US-10-667-295-205
/ Sequence 205, Application US/10667295
/ Publication No. US20050237293A1
/ GENERAL INFORMATION:
/ APPLICANT: Macclia, Peter
/ TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEMS
/ FILE REFERENCE: 11696-047001
/ CURRENT APPLICATION NUMBER: US/10/667,295
/ CURRENT FILING DATE: 2003-09-17
/ PRIOR APPLICATION NUMBER: US 60/411,823
/ PRIOR FILING DATE: 2002-09-17
/ NUMBER OF SEQ ID NOS: 263
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 205
/ LENGTH: 540
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (1)...(540)
/ OTHER INFORMATION: Ceres Seq. ID no. 12450441
US-10-667-295-205

```

Query Match	16.7%;	Score 398;	DB 6;	Length 540;
Best Local Similarity	27.1%;	Pred. No. 2.1e-37;		
Matches 132; Conservative	77;	Mismatches 220;	Indels 58;	Gaps 18;

[illegible]

RESULT 4

US-10-667-295-140
 ; Sequence 140, Application US/10667295
 ; Publication No. US20050257293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mascia, Peter
 ; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
 ; FILE REFERENCE: 11696-047001
 ; CURRENT APPLICATION NUMBER: US/10/667,295
 ; PRIOR FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: US 60/411,823
 ; PRIOR FILING DATE: 2002-09-17
 ; NUMBER OF SEQ ID NOS: 263
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 140
 ; LENGTH: 506
 ; TYPE: PRF
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(506)
 ; OTHER INFORMATION: Ceres Seq. ID no. 13531807
 ; US-10-667-295-140

Query Match 16.2%; Score 387.5; DB 6; Length 506;
 Best Local Similarity 26.5%; Pred. No. 3e-36;
 Matches 135; Conservative 73; Mismatches 227; Indels 75; Gaps 15;

35 PPSXPRLPFIQXHLKDKLHYAXIDLSKKGFLFSXFGSMPTVASTPELFLQ 94
 34 PPGPLP-VPIFGNMLQVGDLDNHRNLTDLAKKFGDIFLLRMGQRLVAVSSPELAKEVHL 92
 95 XKEATSFYTRFQTSAXRXYTD-----XXVAXXKPGYKXFRKLIINDLNATTVXKL 148
 93 -TQGVFSGR-----TRNVVFDIFPGKQDWFVTVYGEHMRKRRIM-----TVPPF 138
 149 RPLRTQQR-----KXLRMAQXAEAKKPLDTEELLKXNSTDYSMMXLGAEABE 197
 139 TNKVVOQYRHGSEEAAYVEDVKNPDAVSGTVIRRLQLMRYNNMTRIMFDRFSE 198
 198 IRDIAREVLKIXG-----EYSLTDFIXPLK-----XLKVGXEKRIIDILNKFPDV 243
 199 EDPIDQLRALNGERSRLAOSFEVYNGDFIPILRPLKGYLKICEVETRLKLFQDYFV 258
 244 VERVTKRRXIVRRXNGEXXGEXSGVXLDTLFEADETXEIKTKXXIXGLVVDXS 303
 259 DER--KKLGSTKSTNNNNE-----LKCAIDHILDAQRKGEINEDNVLYIVENINV 306
 304 AGXDSFAXXTTEWMLAELINNPVYLXXAREEXSVGKDXLVEVPTQNLPIYRAIVKETE 363
 307 AAIETTLMSIEWGIALVNHPEIQQLRDEIDRVLAGHQVTEPDQKLPYLAOVVXETL 366
 364 RHMPLP-VVKRCKXEECKXINGXVXPEGALXXFNWQVQXDXKXYWDRPSEKPERFLETX 422
 367 RLKMAIPLVPHNMHLDAKLGVDIPABSKILVNAMWLANNPAMHMKKPEFRPERFE-- 424
 423 AEGEAXXLDLRGXHFQLLPFGSGRXCPCGVXLTSGXATLLASLIQCFDVLQVGGQQL 482
 425 ---EESLVANNGNDPFLYFPGVGRSCPGIILALPLIGITLRLVONFEL--LPPGQ-- 477
 483 KXDAKVSMEERAG---LTVBRAHSLVCVP 509
 478 ---SQIDTSEKGGQFSHLHLKSTIVAKP 503

RESULT 5

US-10-667-295-139
 ; Sequence 139, Application US/10667295
 ; Publication No. US20050257293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mascia, Peter
 ; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM

FILE REFERENCE: 11696-047001

;; CURRENT APPLICATION NUMBER: US/10/667,295
 ;; CURRENT FILING DATE: 2003-09-17
 ;; PRIOR APPLICATION NUMBER: US 60/411,823
 ;; PRIOR FILING DATE: 2002-09-17
 ;; NUMBER OF SEQ ID NOS: 263
 ;; SOFTWARE: FastSeq for Windows Version 4.0
 ;; SEQ ID NO 139
 ;; LENGTH: 526
 ;; TYPE: PRF
 ;; ORGANISM: Glycine max
 ;; FEATURE:
 ;; NAME/KEY: VARIANT
 ;; LOCATION: (1)...(526)
 ;; OTHER INFORMATION: Ceres Seq. ID no. 13531806
 ; US-10-667-295-139

Query Match 16.2%; Score 387.5; DB 6; Length 526;
 Best Local Similarity 26.5%; Pred. No. 3.2e-36;
 Matches 135; Conservative 73; Mismatches 227; Indels 75; Gaps 15;

35 PPSXPRLPFIQXHLKDKLHYAXIDLSKKGFLFSXFGSMPTVASTPELFLQ 94
 54 PPGPLP-VPIFGNMLQVGDLDNHRNLTDLAKKFGDIFLLRMGQRLVAVSSPELAKEVHL 112
 95 XKEATSFYTRFQTSAXRXYTD-----XXVAXXKPGYKXFRKLIINDLNATTVXKL 148
 113 -TQGVFSGR-----TRNVVFDIFPGKQDWFVTVYGEHMRKRRIM-----TVPPF 158
 149 RPLRTQQR-----KXLRMAQXAEAKKPLDTEELLKXNSTDYSMMXLGAEABE 197
 159 TNKVVOQYRHGSEEAAYVEDVKNPDAVSGTVIRRLQLMRYNNMTRIMFDRFSE 218
 198 IRDIAREVLKIXG-----EYSLTDFIXPLK-----XLKVGXEKRIIDILNKFPDV 243
 219 EDPIDQLRALNGERSRLAOSFEVYNGDFIPILRPLKGYLKICEVETRLKLFQDYFV 278
 244 VERVTKRRXIVRRXNGEXXGEXSGVXLDTLFEADETXEIKTKXXIXGLVVDXS 303
 279 DER--KKLGSTKSTNNNNE-----LKCAIDHILDAQRKGEINEDNVLYIVENINV 326
 304 AGXDSFAXXTTEWMLAELINNPVYLXXAREEXSVGKDXLVEVPTQNLPIYRAIVKETE 363
 327 AAIETTLMSIEWGIALVNHPEIQQLRDEIDRVLAGHQVTEPDQKLPYLAOVVXETL 386
 364 RHMPLP-VVKRCKXEECKXINGXVXPEGALXXFNWQVQXDXKXYWDRPSEKPERFLETX 422
 387 RLKMAIPLVPHNMHLDAKLGVDIPABSKILVNAMWLANNPAMHMKKPEFRPERFE-- 444
 423 AEGEAXXLDLRGXHFQLLPFGSGRXCPCGVXLTSGXATLLASLIQCFDVLQVGGQQL 482
 445 ---EESLVANNGNDPFLYFPGVGRSCPGIILALPLIGITLRLVONFEL--LPPGQ-- 497
 483 KXDAKVSMEERAG---LTVBRAHSLVCVP 509
 498 ---SQIDTSEKGGQFSHLHLKSTIVAKP 523

RESULT 6

US-10-667-295-82
 ; Sequence 82, Application US/10667295
 ; Publication No. US20050257293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mascia, Peter
 ; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
 ; FILE REFERENCE: 11696-047001
 ; CURRENT APPLICATION NUMBER: US/10/667,295
 ; PRIOR FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: US 60/411,823
 ; PRIOR FILING DATE: 2002-09-17
 ; NUMBER OF SEQ ID NOS: 263
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 82

```

; LENGTH: 505
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(505)
; OTHER INFORMATION: Ceres Seq. ID no. 12558791
US-10-667-295-82

Query Match          16.0%; Score 381.5; DB 6; Length 505;
Best Local Similarity 26.1%; Pred. No. 1.5e-35;
Matches 137; Conservative 82; Mismatches 236; Indels 69; Gaps 19;

Oy 1 MLELIALGLXVALFXHLRPTXAXSKALRHLNPPSPXPRLPFIQHXHLLDKLLHYAX 60
Db 4 LLELSL-----IAVAVAILATVISKLKRGKLLKLPFGPILP-IPFGNMLQVDDLNHRL 58
Oy 61 IDLSKKHGPLFSXXFGSMPTVVASSTPELFLQXXEATSFYTRFQTSAXRLTYD---- 116
Db 59 VDYAKKFGDLFLRMGQRNLVVSSPDLTKEVL-LTQVVEFGSR-----TRNVVFDITG 112
Oy 117 --XXVAXXPXPGYKFXFKLIMNDLXNATVYXKLRLRQOIRKCLR-XMAQXAEAXK-- 171
Db 113 KGQDMVFTVYGEHMKRKRIM-----TVPFNNKVQQRBEQMEFEAASVVEDVXKN 164
Oy 172 PLDXTE-----ELKMXNSTXSMXKLGAEIRDIAREVLKIXG-----EYSL 214
Db 165 PDSATKGIVLKRRLQLMYNNMFRIMPDRESEDDPLFLRLKALNGERSRLAQSFEYNY 224
Oy 215 TDFIXPLKXKLVGKYEKRIIDILNKFPDIVER-VIKKRXIVRRXNGEXXEGXSGVYL 273
Db 225 GDFILPLRPLRG-YLKICQDVKDRRIALFKKYFVDERKQJASSKPTG---SEGKCAI 279
Oy 274 DTLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAXXTMALAEILNNPXLXAREE 333
Db 280 DHILE-AEQKG--EINENNVLIYVENINVAIETLWSIENGIAELVNHHPISQKLRNE 335
Oy 334 XYSVVGKXLLVDEVDTONLPYIRAIIVKETPFMAHPPLP-VVKRCKEBCXKNGXVPEGAL 392
Db 336 LDTVIGPQVQVTEPDLHKLPLYQAVVKETLRLRMAIPLLVPHMMLHDAKLAGYDIPASBK 395
Oy 393 XXFNWQVGXDKXKWDPRSEKXPERPLETXABGEAXXLDLRGXHFQLLPFGSGRXMCPGV 452
Db 396 ILVNAWMVLANNPNSWKKEEERPERFE-----ESHVNEANGNDRIYVPFGVGRSCEGT 450
Oy 453 XLATSGXATLLASLLQCFDLOVLGPGQILKXDAKVSMEERAG 496
Db 451 ILALPILGITIGRMVQNFEL-LPPGQ-----SKVDTSKGG 486

RESULT 7
US-10-667-295-81
; Sequence 81, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(534)
; OTHER INFORMATION: Ceres Seq. ID no. 12558790
US-10-667-295-81
```

```

Query Match          16.0%; Score 381.5; DB 6; Length 534;
Best Local Similarity 26.1%; Pred. No. 1.5e-35;
Matches 137; Conservative 82; Mismatches 236; Indels 69; Gaps 19;

Oy 1 MLELIALGLXVALFXHLRPTXAXSKALRHLNPPSPXPRLPFIQHXHLLDKLLHYAX 60
Db 33 LLELSL-----IAVAVAILATVISKLKRGKLLKLPFGPILP-IPFGNMLQVDDLNHRL 87
Oy 61 IDLSKKHGPLFSXXFGSMPTVVASSTPELFLQXXEATSFYTRFQTSAXRLTYD---- 116
Db 88 VDYAKKFGDLFLRMGQRNLVVSSPDLTKEVL-LTQVVEFGSR-----TRNVVFDITG 141
Oy 117 --XXVAXXPXPGYKFXFKLIMNDLXNATVYXKLRLRQOIRKCLR-XMAQXAEAXK-- 171
Db 142 KGQDMVFTVYGEHMKRKRIM-----TVPFNNKVQQRBEQMEFEAASVVEDVXKN 193
Oy 172 PLDXTE-----ELKMXNSTXSMXKLGAEIRDIAREVLKIXG-----EYSL 214
Db 194 PDSATKGIVLKRRLQLMYNNMFRIMPDRESEDDPLFLRLKALNGERSRLAQSFEYNY 253
Oy 215 TDFIXPLKXKLVGKYEKRIIDILNKFPDIVER-VIKKRXIVRRXNGEXXEGXSGVYL 273
Db 254 GDFILPLRPLRG-YLKICQDVKDRRIALFKKYFVDERKQJASSKPTG---SEGKCAI 308
Oy 274 DTLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAXXTMALAEILNNPXLXAREE 333
Db 309 DHILE-AEQKG--EINENNVLIYVENINVAIETLWSIENGIAELVNHHPISQKLRNE 364
Oy 334 XYSVVGKXLLVDEVDTONLPYIRAIIVKETPFMAHPPLP-VVKRCKEBCXKNGXVPEGAL 392
Db 365 LDTVIGPQVQVTEPDLHKLPLYQAVVKETLRLRMAIPLLVPHMMLHDAKLAGYDIPASBK 424
Oy 393 XXFNWQVGXDKXKWDPRSEKXPERPLETXABGEAXXLDLRGXHFQLLPFGSGRXMCPGV 452
Db 425 ILVNAWMVLANNPNSWKKEEERPERFE-----ESHVNEANGNDRIYVPFGVGRSCEGT 479
Oy 453 XLATSGXATLLASLLQCFDLOVLGPGQILKXDAKVSMEERAG 496
Db 480 ILALPILGITIGRMVQNFEL-LPPGQ-----SKVDTSKGG 515

RESULT 8
US-10-667-295-141
; Sequence 141, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 434
; TYPE: PRT
; ORGANISM: glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(434)
; OTHER INFORMATION: Ceres Seq. ID no. 13531808
US-10-667-295-141

Query Match          13.7%; Score 327; DB 6; Length 434;
Best Local Similarity 25.6%; Pred. No. 1.9e-29;
Matches 120; Conservative 68; Mismatches 207; Indels 74; Gaps 14;

Oy 76 GSPFVYASTPELFLQXXEATSFYTRFQTSAXRLTYD-----XXVAXXPXPGPYWX 129
Db 2 GORNVLVVSSPELAKVLAH-LTQVVEFGSR-----TRNVVFDITGKGQDMVFTVYGEHMR 55
```

QY 130 FVRKLIIMNDLXNATVYXKLRPLRTOQIR-----KCLRMAOXAAXKPLDXTEE 178
 Db 56 KMRIM-----TVPFPTKVVQYRNGHSEAAVVEDVKMPDAVSGTVRRRLQ 107
 QY 179 LTKWNSTXSMXKLGEABEIRDIAREVLKIXG-----EYSLTDFIXPK-----XL 224
 Db 108 LMYNNMRYIMFDRPESEDEPIFORLRLNGERSRLAQSPFYNGDFIPILRPFELKGLV 167
 QY 225 KYGXEKRIIDILNKDPVVERVYKGRXIYVRKXNGEXXEGXGVALDTLLEFREDT 284
 Db 168 KICEKVEKTRKLFXQYFEDER--KKLGSTKSTNNNE-----LKCAIDHLLDQ 215
 QY 285 XEIKITKXXIXGLVVDXFSAGDSTAXXTEMALAEINNXPVLXXAREXYSVNGKDXLV 344
 Db 216 RKGELNEDVLYIVENINVAIETTLMSJEMGIAELVNHPEIQOKLRDIDVLGAGHOV 275
 QY 345 DEVDTONLPYIRAIYKETERMHPPLP-VVKRKCCEBXCKINGXVPEGALXXFNWQVQXD 403
 Db 276 TEBDIOKLPYQAVVETIRLMAIPLVPHNMLHDAKLGVDIPAESKILVNAMMLANN 335
 QY 404 XRYWDRPSEKRPRLFETAYAGEAXXLDLRGAHFOLLPGSGRXMCPGYXATLSCXATLL 463
 Db 336 PAHWKKEEPRERPE-----EESLVEANGDFRYLPGVGRSCPGIILALPILGITL 390
 QY 464 ASLQCFDLOVLGPOQOILKGDARXSMERAG--LTVBRAHSLVCVP 509
 Db 391 GRVLONFEL--LPPGQ-----SQIDTSBKGSQFSLHLIKSTIVAKP 431

RESULT 9

US-10-667-295-83
 / Sequence 83, Application US/10667295
 / Publication No. US2005025723A1
 / GENERAL INFORMATION:
 / APPLICANT: Maecia, Peter
 / TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
 / FILE REFERENCE: 11696-047001
 / CURRENT APPLICATION NUMBER: US/10/667,295
 / CURRENT FILING DATE: 2003-09-17
 / PRIOR APPLICATION NUMBER: US 60/411,823
 / PRIOR FILING DATE: 2002-09-17
 / NUMBER OF SEQ ID NOS: 263
 / SOFTWARE: FaastSeq for Windows Version 4.0
 / SEQ ID NO 83
 / LENGTH: 433
 / TYPE: PRF
 / ORGANISM: Arabidopsis thaliana
 / FEATURE:
 / NAME/KEY: VARIANT
 / LOCATION: (1)...(433)
 / OTHER INFORMATION: Ceres Seq. ID no. 12558792
 US-10-667-295-83

Query Match 13.3%; Score 317; DB 6; Length 433;
 Best Local Similarity 25.6%; Pred. No. 2.5e-28; Indels 64; Gaps 17;
 Matches 115; Conservative 71; Mismatches 189;

QY 76 GSNPTVASTPELFLQXXEATSFYTRPOTSAXRLTYD-----XVAXXEXGXYW 129
 Db 2 GORLVVSSPDLTKVEL-LTQVEFGSR-----TRVVFDIFGKGQDMFWYVGBHR 55
 QY 130 FVRKLIIMNDLXNATVYXKLRPLRTOQIRKXLR-XMAOXAAXK--PLDXTE-----E 178
 Db 56 KMRIM-----TVPFPTKVVQYRNGHSEAAVVEDVKMPDAVSGTVRRRLQ 107
 QY 179 LTKWNSTXSMXKLGEABEIRDIAREVLKIXG-----EYSLTDFIXPKLVKGY 229
 Db 108 LMYNNMRYIMFDRPESEDEPIFORLRLNGERSRLAQSPFYNGDFIPILRPFELG-X 166
 QY 230 EKRIIDILNKDPVVER-VIKGRXIYVRKXNGEXXEGXGVALDTLLEFABEYK 288
 Db 167 KICEKVEKTRIALFKYFVDERKQIASKEPTG-----SEGLKCAIDHLE-ABOKG--E 218

QY 289 ITKXXIXGLVVDXFSAGDSTAXXTEMALAEINNXPVLXXAREXYSVNGKDXLVDEVD 348
 Db 219 INEDVLYIVENINVAIETTLMSJEMGIAELVNHPEIQOKLRDIDVLGAGHOVTEPD 278
 QY 349 TONLPYIRAIYKETERMHPPLP-VVKRKCCEBXCKINGXVPEGALXXFNWQVQXDXYW 407
 Db 279 LHKRPYQAVVETIRLMAIPLVPHNMLHDAKLAGVDIPAESKILVNAMMLANNPMSW 338
 QY 408 DRPSEKRPRLFETAYAGEAXXLDLRGAHFOLLPGSGRXMCPGYXATLSCXATLLASLI 467
 Db 339 KPEERFRERPE-----EESLVEANGDFRYLPGVGRSCPGIILALPILGITGMV 393
 QY 468 QCFDLOVLGPOQOILKGDARXSMERAG 496
 Db 394 QNFEL--LPPGQ-----SKVDTSBKGS 414

RESULT 10

US-10-821-234-1554
 / Sequence 1554, Application US/10821234
 / Publication No. US20050255114A1
 / GENERAL INFORMATION:
 / APPLICANT: Labat, Ivan
 / APPLICANT: Stache-Crain, Birgit
 / APPLICANT: Andamant, Susan
 / APPLICANT: Tang, Y. Tom
 / TITLE OF INVENTION: Methods for Diagnosis and Treatment of preclampsia
 / FILE REFERENCE: 821A
 / CURRENT APPLICATION NUMBER: US/10/821,234
 / CURRENT FILING DATE: 2004-04-07
 / PRIOR APPLICATION NUMBER: US 60/462,047
 / PRIOR FILING DATE: 2003-04-07
 / NUMBER OF SEQ ID NOS: 1704
 / SOFTWARE: pt_seq_genes Version 1.0
 / SEQ ID NO 1554
 / LENGTH: 502
 / TYPE: PRF
 / ORGANISM: Homo sapiens
 US-10-821-234-1554

Query Match 10.1%; Score 240.5; DB 6; Length 502;
 Best Local Similarity 22.3%; Pred. No. 1.5e-19; Indels 73; Gaps 20;
 Matches 120; Conservative 83; Mismatches 261;

QY 6 ALGLXVLAFLXHLRPT-----XAXSKALRHLPN--PSPXPRLPFIQHLLKDK 54
 Db 4 AMGSLAALMAVYVHPTLLGLTVAFLAADFLKRRPRKXVPPGPM-RLPFLGNFVLVDFE 62
 QY 55 LHYAXIDLSKKGHPLFSXXFGSMPTVASTPELFLQXXEATSFYTRPOTSAXRXL 114
 Db 63 QSHLEVQGLVKKYKGNFSLJELGDISAVLITGLPLIEALIHMD-QNFGNR-PVTPMBEHT 120
 QY 115 YDXVAXXEXGXYWVVRKLIIMNDLXNATVYXKLRPLRTOQIRKXLRMAO-XAAXK-- 171
 Db 121 FKNGLIMSSGQAMKSORRFTLLALNF-----GLGKSLERLOEEOHLETAIKER 173
 QY 172 ---PLXTEELTKWNSTXSMXKLGEABEIRDI-AREVLKIXGEYSLTDFIXPKLVK 227
 Db 174 NGQFPDPHFKNNAVSNITISITFGBRPEVQDSWFOQLKLDDEVYVLEASKTCQLYNV 233
 QY 228 KYEKRIDILNKDPVVERVY--KRRXIV-----RRXNGEXXEGXGVALDTLLE 278
 Db 234 PW-----IMKFLPGHQTLFSNMKKLKLFSVSHMIDKHKDWNPASTRD---FIDAYLK 283
 QY 279 FADDTYK--IKTKXXIXGLVVDXFSAGDSTAXXTEMALAEINNXPVLXXAREXYS 336
 Db 284 EMSKHTGNPTSSFHEENLISCTLDLPAGTETITLRLMALLMAYLPEIQEKVQAEIDR 343
 QY 337 VVGKDXLVDEVDTONLPYIRAIYKETERMHPPLP-VVKRKCCEBXCKINGXVPEGALXXF 395
 Db 344 VIOGQGPQPSAARESMPTVAIVHEVQRMGNIIFLVNPREVTDTLAGYHLPRGTWILT 403


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QY 109 AXRLTYDXVAXXP-----XGPYXEVFRKLIMNDLXNATVNXLRPLRTQOIRKX 159
Db 128 -----LKWLGEGILLSGDDKMSRRRR-----LTPAFHFNILKSYIT-IFNKS 170
QY 160 LKXMAQ-----XAEAKKPLDYTEELLKMXNSTXSMXGAEAE-IRDIAREVLKIXGEYS 213
Db 171 ANIMLDKQOHLASBESSRLDMFEHI-----SLMTLDSLOKCIFSPDSHCQERPERSEYI 222
QY 214 LTDFTXPLKXKLVKYEKRIDILINKFP-----PVERVYIKKRRX 253
Db 223 AT--LLELSAL-----VEKRSQHILQHMDFLYLSDGRRFHRACRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEGXSVXLD--TLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAX 311
Db 277 TLPQGIIDFFKDKAKSKTLDFIDVLLSKDEGK-ALSDEDIAREADTFMGCHDTTAS 335
QY 312 XTEWALAEILINNPXYLXXAREXYSVVGKXLVDEV--DTONLPIYIRAIYKETFRMHP 368
Db 336 GLSWLYNLARHPEVOERCROEVQELL-KDRDPKEIEMDDLQOLPFLTWCVESIRLHP 394
QY 369 LPVVRKCKXEECKI-NGAXYXPGALXXFNWQVGDXYKWDPRSEKRPERFLETABEGBA 427
Db 395 APFISRCTQDILVLPDGRVYIPKGITCLLDIGVHNHPYVWPDPEVYDPFRFPENSKGRS 454
QY 428 XYLDRGXHFQLLPFGSGRXMCPGVXLATSGXATLLASLIOCF 470
Db 455 -----PLAFIPFSAGFRNCTGQAFPAEMKVVALLMLHF 489

RESULT 13
US-11-000-463-877
; Sequence 877, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 877
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-877
Query Match 8.0%; Score 190; DB 7; Length 524;
```

```
Best Local Similarity 22.0%; Pred. No. 9e-14;
Matches 115; Conservative 63; Mismatches 239; Indels 106; Gaps 21;
QY 1 MLELALGLXVLALEFHLRPPXAXSKALRHLPNPSPXPLPFIQXHL-----LKD 53
Db 20 LLLLVGSMWLA---RLAWTYAFYNNCRLOCFQPPKKNWFWGHLITPTEEGKLD 76
QY 54 KLLHAXIDLSKKGPLEFSXXFGS-MPTVASTBELFLFLOXHA-----TSFXRPQTS 108
Db 77 -----STQMSATYSQGFVWLGPIIPFVLCHPDITISITNASAAAPKONLFIHF-- 127
QY 109 AXRLTYDXVAXXP-----XGPYXEVFRKLIMNDLXNATVNXLRPLRTQOIRKX 159
Db 128 -----LKWLGEGILLSGDDKMSRRRR-----LTPAFHFNILKSYIT-IFNKS 170
QY 160 LKXMAQ-----XAEAKKPLDYTEELLKMXNSTXSMXGAEAE-IRDIAREVLKIXGEYS 213
Db 171 ANIMLDKQOHLASBESSRLDMFEHI-----SLMTLDSLOKCIFSPDSHCQERPERSEYI 222
QY 214 LTDFTXPLKXKLVKYEKRIDILINKFP-----PVERVYIKKRRX 253
Db 223 AT--LLELSAL-----VEKRSQHILQHMDFLYLSDGRRFHRACRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEGXSVXLD--TLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAX 311
Db 277 TLPQGIIDFFKDKAKSKTLDFIDVLLSKDEGK-ALSDEDIAREADTFMGCHDTTAS 335
QY 312 XTEWALAEILINNPXYLXXAREXYSVVGKXLVDEV--DTONLPIYIRAIYKETFRMHP 368
Db 336 GLSWLYNLARHPEVOERCROEVQELL-KDRDPKEIEMDDLQOLPFLTWCVESIRLHP 394
QY 369 LPVVRKCKXEECKI-NGAXYXPGALXXFNWQVGDXYKWDPRSEKRPERFLETABEGBA 427
Db 395 APFISRCTQDILVLPDGRVYIPKGITCLLDIGVHNHPYVWPDPEVYDPFRFPENSKGRS 454
QY 428 XYLDRGXHFQLLPFGSGRXMCPGVXLATSGXATLLASLIOCF 470
Db 455 -----PLAFIPFSAGFRNCTGQAFPAEMKVVALLMLHF 489

RESULT 14
US-11-000-463-878
; Sequence 878, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
```

; PRIOR FILING DATE: 2000-09-15
 ; NUMBER OF SEQ ID NOS: 944
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 878
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-000-463-878

Query Match 8.0%; Score 190; DB 7; Length 524;
 Best Local Similarity 22.0%; Pred. No. 9e-14;
 Matches 115; Conservative 63; Mismatches 239; Indels 106; Gaps 21;

```

QY 1 MLELALGLXVLAFLPHLRPTPXAXSKALRHLNPNPSPXPRLPTIGXHL-----LKD 53
DB 20 LLLLLVGSWMLA---RIIAWTYAFYNNCRRLQCFPPKRWKFWGHLGLITPTEGLKD 76
QY 54 KLLHYAXIDLSSKGGPLPSXKFGS-MPTVVASTEPFLKFLQXXEA---TSFXTRFQTS 108
DB 77 -----STQMSATYSGQFTVMIGPITIPVLCHPDTIRISTNASAAIAPKDLFTRF--- 127
QY 109 AKRXLTIDXXVAXXP-----XGPYXKPVKXLIIMDLXNATVNNKLRPRTQOIRKX 159
DB 128 -----LKPWLGEGILLSGGDKWSRRHRM---LTPAFHFNILKSYIT-IFNKS 170
QY 160 LRXXMQ-----XAEAKKPLDXTTELLKMXNSTXSMXKLGAEAE-IRDIAREVLKIXGEYS 213
DB 171 ANIMLDKWOHLASEGSSCLDMFEHI-----SLMTLDSLOKCIFFSPSHCOERPEYI 222
QY 214 LTFDIXPLKXKLVKGYEKRIDIDILNKFD-----PVVERVKKRRX 253
DB 223 AT--LLELSAL---VEKRSQHILQHMDFLYLISHDGRFRHRCRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEXSGVXLD--TLLEPADETXEIKTKXXIXGLVNDXFSAGXDSTAX 311
DB 277 TLPFGIDDFPKDKAKSKTLDIDVLLSKDEBCK-ALSDEDIRAEADTFMGCHDTTAS 335
QY 312 XTEWALAEILINNPVYLXAXREXYSVGGDXLVDEV---DTQNLPIRAIVKETFPMHP 368
DB 336 GLSWVLVNLARHPEYQERCRQEVQELL-KDRDPKEIEMWDLAQLPFLWCVESIRLHP 394
QY 369 LPVVRKCKXEECKI-NGVXVPEGALXXFNWQVGDXXKWDPRSEKRPRLFETAAEGEA 427
DB 395 APFISRCTQDIDLDPDGRVTPKGITCLDIIIGVHNPTWMPDEVYDPRFPENSKGS 454
QY 428 XXLDLRGXHFQLLPFGSGRXMCPGVXLTATSGXATLLASLIQCF 470
DB 455 -----PLAFIPPSAGPRNCIGQAFMAEMKVVIALMLHF 489

```

RESULT 15

US-11-000-463-879
 ; Sequence 879, Application US/11000463
 ; Publication No. US20050266423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Cao, Yi-Cheng
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 785CIP4CN
 ; CURRENT APPLICATION NUMBER: US/11/000,463
 ; PRIOR FILING DATE: 2004-11-29
 ; PRIOR APPLICATION NUMBER: 10/291,265
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623

; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/922,279
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: 09/491,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 09/617,746
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 09/631,451
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 09/633,870
 ; PRIOR FILING DATE: 2000-09-15
 ; NUMBER OF SEQ ID NOS: 944
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 879
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-000-463-879

Query Match 8.0%; Score 190; DB 7; Length 524;
 Best Local Similarity 22.0%; Pred. No. 9e-14;
 Matches 115; Conservative 63; Mismatches 239; Indels 106; Gaps 21;

```

QY 1 MLELALGLXVLAFLPHLRPTPXAXSKALRHLNPNPSPXPRLPTIGXHL-----LKD 53
DB 20 LLLLLVGSWMLA---RIIAWTYAFYNNCRRLQCFPPKRWKFWGHLGLITPTEGLKD 76
QY 54 KLLHYAXIDLSSKGGPLPSXKFGS-MPTVVASTEPFLKFLQXXEA---TSFXTRFQTS 108
DB 77 -----STQMSATYSGQFTVMIGPITIPVLCHPDTIRISTNASAAIAPKDLFTRF--- 127
QY 109 AKRXLTIDXXVAXXP-----XGPYXKPVKXLIIMDLXNATVNNKLRPRTQOIRKX 159
DB 128 -----LKPWLGEGILLSGGDKWSRRHRM---LTPAFHFNILKSYIT-IFNKS 170
QY 160 LRXXMQ-----XAEAKKPLDXTTELLKMXNSTXSMXKLGAEAE-IRDIAREVLKIXGEYS 213
DB 171 ANIMLDKWOHLASEGSSCLDMFEHI-----SLMTLDSLOKCIFFSPSHCOERPEYI 222
QY 214 LTFDIXPLKXKLVKGYEKRIDIDILNKFD-----PVVERVKKRRX 253
DB 223 AT--LLELSAL---VEKRSQHILQHMDFLYLISHDGRFRHRCRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEXSGVXLD--TLLEPADETXEIKTKXXIXGLVNDXFSAGXDSTAX 311
DB 277 TLPFGIDDFPKDKAKSKTLDIDVLLSKDEBCK-ALSDEDIRAEADTFMGCHDTTAS 335
QY 312 XTEWALAEILINNPVYLXAXREXYSVGGDXLVDEV---DTQNLPIRAIVKETFPMHP 368
DB 336 GLSWVLVNLARHPEYQERCRQEVQELL-KDRDPKEIEMWDLAQLPFLWCVESIRLHP 394
QY 369 LPVVRKCKXEECKI-NGVXVPEGALXXFNWQVGDXXKWDPRSEKRPRLFETAAEGEA 427
DB 395 APFISRCTQDIDLDPDGRVTPKGITCLDIIIGVHNPTWMPDEVYDPRFPENSKGS 454
QY 428 XXLDLRGXHFQLLPFGSGRXMCPGVXLTATSGXATLLASLIQCF 470
DB 455 -----PLAFIPPSAGPRNCIGQAFMAEMKVVIALMLHF 489

```

Search completed: December 22, 2005, 00:16:06
 Job time : 46 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model
Run on: December 21, 2005, 23:57:55 ; Search time 114 Seconds
(without alignments)
1909.553 Million cell updates/sec

Title: US-09-857-581b-66
Perfect score: 2389
Sequence: 1 MLEIALGLXVIALFXHLRP.....ASHIVCVLARIQVASKILLS 521

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main: *
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep: *
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep: *
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep: *
4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep: *
5: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep: *
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2259	94.6	521	US-10-732-923-24073	Sequence 24073, A
2	2257	94.5	521	US-10-732-923-1112	Sequence 1112, Ap
3	2257	94.5	521	US-10-732-923-24055	Sequence 24055, A
4	2257	94.5	521	US-10-732-923-24057	Sequence 24057, A
5	2257	94.5	522	US-10-732-923-24054	Sequence 24054, A
6	2256	94.4	521	US-10-310-154-735	Sequence 735, App
7	2256	94.4	521	US-10-732-923-648	Sequence 648, App
8	2256	94.4	521	US-10-732-923-24056	Sequence 24056, A
9	2250	94.2	521	US-10-659-755-2	Sequence 2, Appl1
10	2248	94.1	521	US-10-505-145-4	Sequence 4, Appl1
11	2178	91.2	500	US-10-732-923-1100	Sequence 1100, Ap
12	2175	91.0	500	US-10-732-923-1102	Sequence 1102, Ap
13	2174	91.0	500	US-10-732-923-1103	Sequence 1103, Ap
14	2173	91.0	500	US-10-732-923-1101	Sequence 1101, Ap
15	2173	91.0	500	US-10-732-923-1082	Sequence 1082, A
16	2172	90.9	500	US-10-732-923-1087	Sequence 1087, Ap
17	2172	90.9	500	US-10-732-923-1099	Sequence 1099, Ap
18	2172	90.9	500	US-10-732-923-24070	Sequence 24070, A
19	2171	90.9	500	US-10-732-923-1105	Sequence 1105, Ap
20	2169	90.8	499	US-10-732-923-1104	Sequence 1104, Ap
21	2163	90.5	499	US-10-732-923-1083	Sequence 1083, Ap
22	2140	89.6	521	US-10-732-923-24074	Sequence 24074, A
23	2130	89.2	511	US-10-739-930-9041	Sequence 9041, Ap
24	1969.5	82.4	523	US-10-732-923-24088	Sequence 24088, A
25	1946	81.5	523	US-10-732-923-24069	Sequence 24069, A
26	1918	80.3	523	US-10-732-923-24072	Sequence 24072, A
27	1896	79.4	518	US-10-732-923-1086	Sequence 1086, Ap

28	1216	50.9	523	US-10-732-923-24089	Sequence 24089, A
29	1212	50.7	523	US-10-732-923-24090	Sequence 24090, A
30	944.5	39.5	512	US-10-411-115-4	Sequence 4, Appl1
31	944.5	39.5	512	US-10-411-115-4	Sequence 4, Appl1
32	940.5	39.4	506	US-10-411-115-2	Sequence 2, Appl1
33	940.5	39.4	506	US-10-411-115-2	Sequence 2, Appl1
34	940.5	39.4	506	US-10-732-923-1107	Sequence 1107, Ap
35	932.5	39.0	511	US-10-732-923-1084	Sequence 1084, Ap
36	921.5	38.6	506	US-10-411-115-8	Sequence 8, Appl1
37	921.5	38.6	506	US-10-411-115-8	Sequence 8, Appl1
38	919.5	38.5	509	US-10-424-599-149724	Sequence 149724, A
39	891.5	37.3	509	US-10-424-599-221409	Sequence 221409, A
40	870	36.4	510	US-10-424-599-263430	Sequence 263430, A
41	843	35.3	502	US-10-437-963-150757	Sequence 150757, A
42	807.5	33.8	579	US-10-437-963-150757	Sequence 150757, A
43	761.5	31.9	518	US-10-437-963-123495	Sequence 123495, A
44	753.5	31.5	518	US-10-732-923-24084	Sequence 24084, A
45	730.5	30.6	516	US-10-437-963-169616	Sequence 169616, A

ALIGNMENTS

RESULT 1
US-10-732-923-24073 Application US/10732923
; Sequence 24073, Appl1cation US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FIDE REFERENCE: 38-15(52786)C
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 24073
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Pisum sativum
US-10-732-923-24073

Query Match 94.6%; Score 2259; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 3,9e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY	1	MLEIALGLXVIALFXHLRPFPXAKSKALRHPNPPSPXPLPFGHXLKDKLHYAX	60
DB	1	MLEIALGLFVIALFLHLPFPSPAKSKALRHPNPPSPXPLPFGHXLKDKLHYAL	60
QY	61	IDLKXGFLFSGXFGSMPTVASTPELFLQXXEATSEFTRPQTSAXRXYLYDXVA	120
DB	61	IDLKXGFLFSLSGSMPTVASTPELFLQXHEATSEFSTRPQTSAXRXYLYDNSVA	120
QY	121	XXPXPGRYKFKLIMNDLXNATTNXLRPLRTOQIRKLRMAQXAEKXRLDXTBEL	180
DB	121	WPFPGYKFKLIMNDLXNATTNELRPLRTOQIRKLRMAQSAEQKPLDVTBEL	180
QY	181	KXNXTXSMXKGEABEIRDIAREVLKIXGSLTDFIXPLKLYGKYEKIDIDLNF	240
DB	181	KMTNSTISMMWGEABEIRDIAREVLKIPGSLTDFIPLKLYGKYEKIDIDLNF	240
QY	241	DPVERVIRKRXIVRRXNGEXGEXGVXLOTLLEFADETXIKITKXXIXGLVVD	300
DB	241	DVVERVIRKREIVRRNGEVEGEASGVLDLTLLBEADETWIKITKXOIXGLVVD	300
QY	301	XKSAGDSTAXXTMALAEINNPPVIXAREBXSVGKDLVBDQNPYIRAIYK	360
DB	301	FPSAGDSTAVATEWALAEINNPPVLOQAREBVSVGKDLVBDVTQNPYIRAIYK	360
QY	361	ETFRMHPPLPVYKRCXECXINGKXPEGALXXFNWVGDXDKXTWDPSEKPERFLE	420
DB	361	ETFRMHPPLPVYKRCXECXINGKXPEGALVLFNWWVGDXDKXTWDPSEKPERFLE	420

QY 421 TXABEAXXLDLRGXHFLPFGSGRXCPCGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 DB 421 TGAEBEAPLDLRGXHFLPFGSGRXCPCGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 QY 481 ILKGDACVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521
 DB 481 ILKGDACVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 2

US-10-732-923-1112
 ; Sequence 1112, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 1112
 ; LENGTH: 521
 ; TYPE: PRT
 ; ORGANISM: Trifolium pratense
 US-10-732-923-1112

Query Match 94.5%; Score 2257; DB 5; Length 521;
 Best Local Similarity 86.8%; Pred. No. 6.7e-256;
 Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLEIALGLXVIALFXHLRPTPXAXSKALRHLNPPSPKRLPFIQHXHLLKDXLHYAX 60
 DB 1 MLEIALGLXVIALFXHLRPTPXAXSKALRHLNPPSPKRLPFIQHXHLLKDXLHYAX 60
 QY 61 IDLSKKGPLFSXXFGSMPTVASTPELFLKFLQXXEATSFXTRFQTSAXKXLYDXXYA 120
 DB 61 IDLSKKGPLFSXXFGSMPTVASTPELFLKFLQXXEATSFXTRFQTSAXKXLYDXXYA 120
 QY 121 XXPXGPVXKFXRKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 DB 121 XXPXGPVXKFXRKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 QY 121 WVPPIPPVWKFVAKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 DB 121 WVPPIPPVWKFVAKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 QY 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 DB 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 QY 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 DB 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 QY 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 DB 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 QY 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 DB 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 QY 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 DB 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 QY 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 DB 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 QY 361 EFRHNPPLPVYKRCXEBXCINGXVXPEGALXXFNWQVGDXXKWPDPSEKXPERPLE 420
 DB 361 EFRHNPPLPVYKRCXEBXCINGXVXPEGALXXFNWQVGDXXKWPDPSEKXPERPLE 420
 QY 421 TXABEAXXLDLRGXHFLPFGSGRXCPCGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 DB 421 TGAEBEAPLDLRGXHFLPFGSGRXCPCGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 QY 481 ILKGDACVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521
 DB 481 ILKGDACVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 3

US-10-732-923-24055
 ; Sequence 24055, Application US/10732923

Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 24055
 ; LENGTH: 521
 ; TYPE: PRT
 ; ORGANISM: Vigna radiata
 US-10-732-923-24055

Query Match 94.5%; Score 2257; DB 5; Length 521;
 Best Local Similarity 86.8%; Pred. No. 6.7e-256;
 Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLEIALGLXVIALFXHLRPTPXAXSKALRHLNPPSPKRLPFIQHXHLLKDXLHYAX 60
 DB 1 MLEIALGLXVIALFXHLRPTPXAXSKALRHLNPPSPKRLPFIQHXHLLKDXLHYAX 60
 QY 61 IDLSKKGPLFSXXFGSMPTVASTPELFLKFLQXXEATSFXTRFQTSAXKXLYDXXYA 120
 DB 61 IDLSKKGPLFSXXFGSMPTVASTPELFLKFLQXXEATSFXTRFQTSAXKXLYDXXYA 120
 QY 121 XXPXGPVXKFXRKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 DB 121 XXPXGPVXKFXRKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 QY 121 WVPPIPPVWKFVAKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 DB 121 WVPPIPPVWKFVAKLIMNDLXNATVNNKLRPLRTOQIRKXLRXMOXAAXKPLDTEELL 180
 QY 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 DB 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 QY 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 DB 181 KXNXTXSMXKLGABEIRDIAREVLKIXGEYSLDFIXPLKXKVGKYEKRIDIDLINKE 240
 QY 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 DB 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 QY 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 DB 241 DPVVERVVKRRKXIVRRXNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 QY 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 DB 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 QY 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 DB 301 XFSAGXDSXTAXXTMALAEILNNPVYLXXAREEYXSVGKXLDVEVDTONLPYIRATVK 360
 QY 361 EFRHNPPLPVYKRCXEBXCINGXVXPEGALXXFNWQVGDXXKWPDPSEKXPERPLE 420
 DB 361 EFRHNPPLPVYKRCXEBXCINGXVXPEGALXXFNWQVGDXXKWPDPSEKXPERPLE 420
 QY 421 TXABEAXXLDLRGXHFLPFGSGRXCPCGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 DB 421 TGAEBEAPLDLRGXHFLPFGSGRXCPCGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 QY 481 ILKGDACVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521
 DB 481 ILKGDACVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 4

US-10-732-923-24057
 ; Sequence 24057, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 24057
 ; LENGTH: 521
 ; TYPE: PRT

ORGANISM: Vigna radiata
US-10-732-923-24057

Query Match 94.5%; Score 2257; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 6.7e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALEFXHLRPTPXAXSKALRHLNPNPSPXPRLPIGIXHLLKDKLLHYAX 60
DB 1 MLELALGLVLALEFLHRLPTPTAKSKALRHLNPNPSPXPRLPIGIXHLLKDKLLHYAL 60
QY 61 IDLSKKGPLPSXFGSMPTVASTPELFLQXXEATSEFTRQTSAXRLTYDXVA 120
DB 61 IDLSKKGPLPSLFGSMPTVASTPELFLQTHEATSEFTRQTSAIRLTYDSSVA 120
QY 121 XXXPAPYKFKVRLIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAEXKPLDTELL 180
DB 121 MVEPBPYKFKVRLIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAEXKPLDTELL 180
QY 181 KXNSTXSMXKGAEEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
DB 181 KXNSTXSMXKGAEEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
QY 181 KXNSTXSMXKGAEEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
DB 181 KXNSTXSMXKGAEEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
QY 241 DEVERVIKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETEIKITKXIXGLVVD 300
DB 241 DEVERVIKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETEIKITKXIXGLVVD 300
QY 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKXLDVDEVTQMLPYIRAVK 360
DB 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKXLDVDEVTQMLPYIRAVK 360
QY 361 EFPFMHPLPVYKRCCKEEXINGXVAPGALXXFNWQVGDXXKXWDRPSEKPERPLE 420
DB 361 EFPFMHPLPVYKRCCKEEXINGXVAPGALXXFNWQVGDXXKXWDRPSEKPERPLE 420
QY 421 TYAEGEAXXLDLRGXHFQLLPFGSGRMCPCGVXLATSGATLLASLIQCFDLOVLGPOQ 480
DB 421 TYAEGEAXXLDLRGXHFQLLPFGSGRMCPCGVXLATSGATLLASLIQCFDLOVLGPOQ 480
QY 481 ILKGDARVSMERAGLTVPRASHLCVPLARIGVASKILLS 521
DB 481 ILKGDARVSMERAGLTVPRASHLCVPLARIGVASKILLS 521

RESULT 5

US-10-732-923-24054
Sequence 24054, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(5796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 24054
LENGTH: 522
TYPE: PRT
ORGANISM: Vigna radiata
US-10-732-923-24054

Query Match 94.5%; Score 2257; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 6.7e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALEFXHLRPTPXAXSKALRHLNPNPSPXPRLPIGIXHLLKDKLLHYAX 60
DB 1 MLELALGLVLALEFLHRLPTPTAKSKALRHLNPNPSPXPRLPIGIXHLLKDKLLHYAL 60
QY 61 IDLSKKGPLPSXFGSMPTVASTPELFLQXXEATSEFTRQTSAXRLTYDXVA 120
DB 61 IDLSKKGPLPSLFGSMPTVASTPELFLQTHEATSEFTRQTSAIRLTYDSSVA 120

DB 61 IDLSKKGPLPSLFGSMPTVASTPELFLQTHEATSEFTRQTSAIRLTYDSSVA 120
QY 121 XXXPAPYKFKVRLIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAEXKPLDTELL 180
DB 121 MVEPBPYKFKVRLIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAEXKPLDTELL 180
QY 181 KXNSTXSMXKGAEEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
DB 181 KXNSTXSMXKGAEEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKRIIDILNKF 240
QY 241 DEVERVIKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETEIKITKXIXGLVVD 300
DB 241 DEVERVIKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETEIKITKXIXGLVVD 300
QY 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKXLDVDEVTQMLPYIRAVK 360
DB 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKXLDVDEVTQMLPYIRAVK 360
QY 361 EFPFMHPLPVYKRCCKEEXINGXVAPGALXXFNWQVGDXXKXWDRPSEKPERPLE 420
DB 361 EFPFMHPLPVYKRCCKEEXINGXVAPGALXXFNWQVGDXXKXWDRPSEKPERPLE 420
QY 421 TYAEGEAXXLDLRGXHFQLLPFGSGRMCPCGVXLATSGATLLASLIQCFDLOVLGPOQ 480
DB 421 TYAEGEAXXLDLRGXHFQLLPFGSGRMCPCGVXLATSGATLLASLIQCFDLOVLGPOQ 480
QY 481 ILKGDARVSMERAGLTVPRASHLCVPLARIGVASKILLS 521
DB 481 ILKGDARVSMERAGLTVPRASHLCVPLARIGVASKILLS 521

RESULT 6

US-10-310-154-735
Sequence 735, Application US/10310154
Publication No. US2003023670A1

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H.
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupalli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinzuo
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shishieh
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A.
APPLICANT: Laccetti, Lucille B.
APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-Yi
APPLICANT: Liu, Jindong
APPLICANT: Lu, Bin
APPLICANT: Luethy, Michael M.
APPLICANT: Madison, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchi Kant
APPLICANT: Parmell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.

APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanqun
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 735
LENGTH: 521
TYPE: PRT
ORGANISM: Glycine max
US-10-310-154-735

Query Match 94.4%; Score 2256; DB 4; Length 521;
Best Local Similarity 86.8%; Pred. No. 8.8e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALEFXHLRPTPXAXSKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60
DB 1 MLELALGLVLALEFLHLRPTTAKSKALRHLPNPSPXPRLPFIQHLHLKDKLHYAL 60
QY 61 IDLSKKGPPLFSXXFGSMPTVASTPELFKFLQXXEATSPYTRFQTSAXKLYDXVA 120
DB 61 IDLSKKGPPLFSLYFGSMPTVASTPELFKFLQTHEATSPYTRFQTSAIRRLTYDSSVA 120
QY 121 XXPGPYMXFVRKLIIMNDLXNATVNNKLRPLRTQOIRKCLRMAQXABKRLDTEELL 180
DB 121 MVEPGPYMKFVRKLIIMNDLXNATVNNKLRPLRTQOIRKCLRMAQABKRLDTEELL 180
QY 181 KMXNSTXSMXKLGAEIIRDIAREVLKIXGEYSLTDFIXPLKXKVKYKRIIDILNKF 240
DB 181 KMTNSTISMMMLGAEBEIRDIAREVLKIFGEYSLTDFIWPDKHVKGYEKRIIDILNKF 240
QY 241 DPVVERVIKKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
DB 241 DPVVERVIKKRRREIVRRKNGEVVEGVSGLDTLLEFADETXEIKITKDHIKGLVVD 300
QY 301 XFSAGXSTAXXTMALAEILNNPVLYXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
DB 301 FFSAGTDSYAVATEMALAEILNNPVLYEXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
QY 361 ETRFMHPLPVYKRCXEECXINGXVXPEGALXFNVMQVGDXXKXWDRPSEXPPEPFL 420
DB 361 ETRFMHPLPVYKRCXEECXINGVYIPEGALILFNVMQVGDPRKXWDRPSEXPPEPFL 420
QY 421 TXAGEAXXLDLRGXHFLPLRPGSGRXCPCVXLATSGXATLLASLIQCFDLQVLGPQG 480
DB 421 TXAGEAGPLDLRGHFLPLRPGSGRXCPCVNLATSGMATLLASLIQCFDLQVLGPQG 480
QY 481 ILKGDADKVSMEERAGLTVPRASHLCVPLARIGVASKLS 521
DB 481 ILKGDADKVSMEERAGLTVPRASHLCVPLARIGVASKLS 521

RESULT 7
US-10-732-923-648
Sequence 648, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154

PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 648
LENGTH: 521
TYPE: PRT
ORGANISM: Glycine max
US-10-732-923-648

Query Match 94.4%; Score 2256; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 8.8e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALEFXHLRPTPXAXSKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60
DB 1 MLELALGLVLALEFLHLRPTTAKSKALRHLPNPSPXPRLPFIQHLHLKDKLHYAL 60
QY 61 IDLSKKGPPLFSXXFGSMPTVASTPELFKFLQXXEATSPYTRFQTSAXKLYDXVA 120
DB 61 IDLSKKGPPLFSLYFGSMPTVASTPELFKFLQTHEATSPYTRFQTSAIRRLTYDSSVA 120
QY 121 XXPGPYMXFVRKLIIMNDLXNATVNNKLRPLRTQOIRKCLRMAQXABKRLDTEELL 180
DB 121 MVEPGPYMKFVRKLIIMNDLXNATVNNKLRPLRTQOIRKCLRMAQABKRLDTEELL 180
QY 181 KMXNSTXSMXKLGAEIIRDIAREVLKIXGEYSLTDFIXPLKXKVKYKRIIDILNKF 240
DB 181 KMTNSTISMMMLGAEBEIRDIAREVLKIFGEYSLTDFIWPDKHVKGYEKRIIDILNKF 240
QY 241 DPVVERVIKKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
DB 241 DPVVERVIKKRRREIVRRKNGEVVEGVSGLDTLLEFADETXEIKITKDHIKGLVVD 300
QY 301 XFSAGXSTAXXTMALAEILNNPVLYXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
DB 301 FFSAGTDSYAVATEMALAEILNNPVLYEXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
QY 361 ETRFMHPLPVYKRCXEECXINGXVXPEGALXFNVMQVGDXXKXWDRPSEXPPEPFL 420
DB 361 ETRFMHPLPVYKRCXEECXINGVYIPEGALILFNVMQVGDPRKXWDRPSEXPPEPFL 420
QY 421 TXAGEAXXLDLRGXHFLPLRPGSGRXCPCVXLATSGXATLLASLIQCFDLQVLGPQG 480
DB 421 TXAGEAGPLDLRGHFLPLRPGSGRXCPCVNLATSGMATLLASLIQCFDLQVLGPQG 480
QY 481 ILKGDADKVSMEERAGLTVPRASHLCVPLARIGVASKLS 521
DB 481 ILKGDADKVSMEERAGLTVPRASHLCVPLARIGVASKLS 521

RESULT 8
US-10-732-24056
Sequence 24056, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 24056
LENGTH: 521
TYPE: PRT
ORGANISM: Vigna radiata
US-10-732-923-24056

Query Match 94.4%; Score 2256; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 8.8e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALEFXHLRPTPXAXSKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60

```

Db      1 MLELALGLVLAFLHLRPTAKSKALRHLNPPSPKRLPFIQHLLKDLKLYAL 60
Qy      61 IDLSKRGPLRSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Db      61 IDLSKRGPLRSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Qy      121 XXPGPYMKFVRKLIIMNDLNATTVNKLRLPTQIRKRLXMAQAAXAKPLDXTBELL 180
Db      121 MWPFGPYMKFVRKLIIMNDLNATTVNKLRLPTQIRKRLXMAQAAXAKPLDXTBELL 180
Qy      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Db      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Qy      241 DPVVRVVKRRKXIVRRKXNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVND 300
Db      241 DPVVRVVKRRKXIVRRKXNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVND 300
Qy      301 XPSAGDSTAXXTWMAELINNPVYLXXAREEYSVVGKDLVDEVDTONLPYIRAIYK 360
Db      301 XPSAGDSTAXXTWMAELINNPVYLXXAREEYSVVGKDLVDEVDTONLPYIRAIYK 360
Qy      361 ETRFMHPLPVYKRCXECXINGVXPEGALXXFNWQVGDXTWDRPSEKRPERFLE 420
Db      361 ETRFMHPLPVYKRCXECXINGVXPEGALXXFNWQVGDXTWDRPSEKRPERFLE 420
Qy      421 TYABEAXXLDLRCGHFOLLPRGSGRMCPGVXLATSGATLASLIQCFDLQVLGPQO 480
Db      421 TYABEAXXLDLRCGHFOLLPRGSGRMCPGVXLATSGATLASLIQCFDLQVLGPQO 480
Qy      481 ILKGDAXVSMERAGLTVPRASHLVCVPLARIGVASKLS 521
Db      481 ILKGDAXVSMERAGLTVPRASHLVCVPLARIGVASKLS 521

```

RESULT 9

```

US-10-659-755-2
; Sequence 2, Application US/10659755
; Publication No. US20040128711A1
; GENERAL INFORMATION:
; APPLICANT: DIXON, RICHARD A.
; APPLICANT: LIU, CHANG-JUN
; APPLICANT: DEAVOURS, BETTINA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
; TITLE OF INVENTION: AND ISOFLAVONOID NUTRACEUTICALS
; FILE REFERENCE: NMLE:007US
; CURRENT APPLICATION NUMBER: US/10/659,755
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,447
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Soybean
US-10-659-755-2

```

Query Match 94.2%; Score 2250; DB 4; Length 521;
 Best Local Similarity 86.6%; Pred. No. 4, 4e-255;
 Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

```

Qy      1 MLELALGLVLAFLHLRPTAKSKALRHLNPPSPKRLPFIQHLLKDLKLYAL 60
Db      1 MLELALGLVLAFLHLRPTAKSKALRHLNPPSPKRLPFIQHLLKDLKLYAL 60
Qy      61 IDLSKRGPLRSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Db      61 IDLSKRGPLRSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Qy      121 XXPGPYMKFVRKLIIMNDLNATTVNKLRLPTQIRKRLXMAQAAXAKPLDXTBELL 180
Db      121 XXPGPYMKFVRKLIIMNDLNATTVNKLRLPTQIRKRLXMAQAAXAKPLDXTBELL 180

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Db      121 MWPFGPYMKFVRKLIIMNDLNATTVNKLRLPTQIRKRLXMAQAAXAKPLDXTBELL 180
Qy      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Db      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Qy      241 DPVVRVVKRRKXIVRRKXNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVND 300
Db      241 DPVVRVVKRRKXIVRRKXNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVND 300
Qy      301 XPSAGDSTAXXTWMAELINNPVYLXXAREEYSVVGKDLVDEVDTONLPYIRAIYK 360
Db      301 XPSAGDSTAXXTWMAELINNPVYLXXAREEYSVVGKDLVDEVDTONLPYIRAIYK 360
Qy      361 ETRFMHPLPVYKRCXECXINGVXPEGALXXFNWQVGDXTWDRPSEKRPERFLE 420
Db      361 ETRFMHPLPVYKRCXECXINGVXPEGALXXFNWQVGDXTWDRPSEKRPERFLE 420
Qy      421 TYABEAXXLDLRCGHFOLLPRGSGRMCPGVXLATSGATLASLIQCFDLQVLGPQO 480
Db      421 TYABEAXXLDLRCGHFOLLPRGSGRMCPGVXLATSGATLASLIQCFDLQVLGPQO 480
Qy      481 ILKGDAXVSMERAGLTVPRASHLVCVPLARIGVASKLS 521
Db      481 ILKGDAXVSMERAGLTVPRASHLVCVPLARIGVASKLS 521

```

RESULT 10

```

US-10-505-145-4
; Sequence 4, Application US/10505145
; Publication No. US20050241014A1
; GENERAL INFORMATION:
; APPLICANT: COLLIVER, Steven Peter
; APPLICANT: DOBB, Roy Thomas
; APPLICANT: van der Hilden, Hendrikus Theodorus Wilhelmus Maria
; TITLE OF INVENTION: PRODUCTION OF DADZEIN IN TRANSGENIC PLANTS
; FILE REFERENCE: 56159-5241
; CURRENT APPLICATION NUMBER: US/10/505,145
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/EP03/01465
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP 02251404.6
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-10-505-145-4

```

Query Match 94.1%; Score 2248; DB 5; Length 521;
 Best Local Similarity 86.4%; Pred. No. 7, 6e-255;
 Matches 450; Conservative 1; Mismatches 70; Indels 0; Gaps 0;

```

Qy      1 MLELALGLVLAFLHLRPTAKSKALRHLNPPSPKRLPFIQHLLKDLKLYAL 60
Db      1 MLELALGLVLAFLHLRPTAKSKALRHLNPPSPKRLPFIQHLLKDLKLYAL 60
Qy      61 IDLSKRGPLRSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Db      61 IDLSKRGPLRSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Qy      121 XXPGPYMKFVRKLIIMNDLNATTVNKLRLPTQIRKRLXMAQAAXAKPLDXTBELL 180
Db      121 MWPFGPYMKFVRKLIIMNDLNATTVNKLRLPTQIRKRLXMAQAAXAKPLDXTBELL 180
Qy      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Db      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Qy      241 DPVVRVVKRRKXIVRRKXNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVND 300
Db      241 DPVVRVVKRRKXIVRRKXNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVND 300

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Db      241 DPEVVERIKKREIVRRKNGVEVGEVFLDTLLEFADEBTWEIKTKDHKIGLVVD 300
Qy      301 XFSAGDSTAXXTXEWALAEIINNPKYLXXAREEXYSVVGKDLVDEVTQNLPIYRAIYK 360
          |||
Db      301 FFSAGTDTAVATWALAEIINNPKYLEKAREEYYSVVGKDLVDEVTQNLPIYRAIYK 360
Qy      361 ETRFMHPPLPVVKRKCEXKINGXVPEGALXXFNWQVGDXYKWRPSEKPERELE 420
          |||
Db      361 ETRFMHPPLPVVKRKCEXKINGXVPEGALILFNWQVGRDPKXWRPSEKPERELE 420
Qy      421 TXABEAXXLDLRGNHFOILLPGSGRMC PGVXLATSGATILASLIQCFDLOVGPQOQ 480
          |||
Db      421 TGAEBEAPDLDRGNHFOILLPGSGRMC PGVNLATSGATILASLIQCFDLOVGPQOQ 480
Qy      481 ILKGDADAKSMERAGLTVPRASHLVCVPLARIIGVASKLS 521
          |||
Db      481 ILKGDADAKSMERAGLTVPRASHLVCVPLARIIGVASKLS 521

```

```

RESULT 11
US-10-732-923-1100
; Sequence 1100, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIORITY FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1100
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Medicago sativa
US-10-732-923-1100

```

```

Query Match      91.2%; Score 2178; DB 5; Length 500;
Best Local Similarity 86.4%; Pred. No. 1,2e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```

```

Qy      15 FXHLRPTXAXSKALRHLNPPSPKRLPFIIGHHLKDKLLHYXIDLSKKHGLFSXX 74
          |||
Db      1 FLHLRPTXAKSKALRHLNPPSPKRLPFIIGHHLKDKLLHYALIDLSKKGGLFSIX 60
Qy      75 FGSMTVVAATPELFLKPLQHXEATSFKTRFOTSAKRLTYDXVAXXPGPYMKFVRKL 134
          |||
Db      61 FGSMTVVAATPELFLKPLQHXEATSFKTRFOTSAKRLTYDXVAXXPGPYMKFVRKL 120
Qy      135 IMNDLXNATTVNKLRLPTQOIRKCLRMAQXAEAKPLDYTEELLKXNSTXSMXKIGE 194
          |||
Db      121 IMNDLXNATTVNKLRLPTQOIRKCLRMAQXAEAKPLDYTEELLKXNSTXSMXKIGE 180
Qy      195 ABEIRDIAREVLKIXGEYSITDFIXPLKXKLVGKYEKRIIDILNKFDPVBERVIKRRXI 254
          |||
Db      181 ABEIRDIAREVLKIXGEYSITDFIXPLKXKLVGKYEKRIIDILNKFDPVBERVIKRRXI 240
Qy      255 VRRRNGEVEGEVGVFLDTLLEFADEBTWEIKTKDHKIGLVVDLFSAGTDTAVATE 300
          |||
Db      241 VRRRNGEVEGEVGVFLDTLLEFADEBTWEIKTKDHKIGLVVDLFSAGTDTAVATE 300
Qy      315 WALAEIINNPKYLXXAREEXYSVVGKDLVDEVTQNLPIYRAIYKTRFMHPPLPVVKR 374
          |||
Db      301 WALAEIINNPKYLEKAREEYYSVVGKDLVDEVTQNLPIYRAIYKTRFMHPPLPVVKR 360
Qy      375 KCXBECKINGXVPEGALXXFNWQVGDXYKWRPSEKPERPLETJABEAXXLDLRG 434
          |||
Db      361 KCTECEINGVYIPGALILFNWQVGRDPSKWRPSEKPERPLETJABEAXXLDLRG 420
Qy      435 XHFOLLPGSGRMC PGVXLATSGATILASLIQCFDLOVGPQOQILKGDADAKSMER 494
          |||
Db      421 OHFOLLPGSGRMC PGVNLATSGATILASLIQCFDLOVGPQOQILKGDADAKSMER 480

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Qy      495 AGLTVPRASHLVCVPLARIIG 514
          |||
Db      481 AGLTVPRASHLVCVPLARIIG 500

```

```

RESULT 12
US-10-732-923-1102
; Sequence 1102, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIORITY FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1102
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Medicago sativa
US-10-732-923-1102

```

```

Query Match      91.0%; Score 2175; DB 5; Length 500;
Best Local Similarity 86.4%; Pred. No. 2,8e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```

```

Qy      15 FXHLRPTXAXSKALRHLNPPSPKRLPFIIGHHLKDKLLHYXIDLSKKHGLFSXX 74
          |||
Db      1 FLHLRPTXAKSKALRHLNPPSPKRLPFIIGHHLKDKLLHYALIDLSKKGGLFSIX 60
Qy      75 FGSMTVVAATPELFLKPLQHXEATSFKTRFOTSAKRLTYDXVAXXPGPYMKFVRKL 134
          |||
Db      61 FGSMTVVAATPELFLKPLQHXEATSFKTRFOTSAKRLTYDXVAXXPGPYMKFVRKL 120
Qy      135 IMNDLXNATTVNKLRLPTQOIRKCLRMAQXAEAKPLDYTEELLKXNSTXSMXKIGE 194
          |||
Db      121 IMNDLXNATTVNKLRLPTQOIRKCLRMAQXAEAKPLDYTEELLKXNSTXSMXKIGE 180
Qy      195 ABEIRDIAREVLKIXGEYSITDFIXPLKXKLVGKYEKRIIDILNKFDPVBERVIKRRXI 254
          |||
Db      181 ABEIRDIAREVLKIXGEYSITDFIXPLKXKLVGKYEKRIIDILNKFDPVBERVIKRRXI 240
Qy      255 VRRRNGEVEGEVGVFLDTLLEFADEBTWEIKTKDHKIGLVVDLFSAGTDTAVATE 300
          |||
Db      241 VRRRNGEVEGEVGVFLDTLLEFADEBTWEIKTKDHKIGLVVDLFSAGTDTAVATE 300
Qy      315 WALAEIINNPKYLXXAREEXYSVVGKDLVDEVTQNLPIYRAIYKTRFMHPPLPVVKR 374
          |||
Db      301 WALAEIINNPKYLEKAREEYYSVVGKDLVDEVTQNLPIYRAIYKTRFMHPPLPVVKR 360
Qy      375 KCXBECKINGXVPEGALXXFNWQVGDXYKWRPSEKPERPLETJABEAXXLDLRG 434
          |||
Db      361 KCTECEINGVYIPGALILFNWQVGRDPSKWRPSEKPERPLETJABEAXXLDLRG 420
Qy      435 XHFOLLPGSGRMC PGVXLATSGATILASLIQCFDLOVGPQOQILKGDADAKSMER 494
          |||
Db      421 OHFOLLPGSGRMC PGVNLATSGATILASLIQCFDLOVGPQOQILKGDADAKSMER 480
Qy      495 AGLTVPRASHLVCVPLARIIG 514
          |||
Db      481 AGLTVPRASHLVCVPLARIIG 500

```

```

RESULT 13
US-10-732-923-1103
; Sequence 1103, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

```

```
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 1103
LENGTH: 500
TYPE: PRT
ORGANISM: Trifolium repens
US-10-732-923-1103
```

```
Query Match          91.0%; Score 2174; DB 5; Length 500;
Best Local Similarity 86.4%; Pred. No. 3,6e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
```

```
QY 15 FxHLRPTPYAXSKALRHLNPNPSPXPRLPFIIGHXHLKDKLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTPYAXSKALRHLNPNPSPXPRLPFIIGHXHLKDKLHYAXIDLKSKHGPLFSLY 60
QY 75 FGSMPVAVASTPELFLFLQTHXATSFYTRFQTSAXRKLTYDXVAXXPXGPMXKFRKL 134
DB 61 FGSMPVAVASTPELFLFLQTHXATSFYTRFQTSAXRKLTYDXVAXXPXGPMXKFRKL 120
QY 135 IMNDLXNATTVNXXLRPLRTQOIRKXLRMAOXAAXKPLDYTELLKMNSTXSMXKIGE 194
DB 121 IMNDLXNATTVNXXLRPLRTQOIRKXLRMAOXAAXKPLDYTELLKMNSTXSMXKIGE 180
QY 195 ABEIRDIAREVLKIXGEYSYLDPIPLKXLRVKGXKRIIDILNKFDPVVERVIKRRXI 254
DB 181 ABEIRDIAREVLKIXGEYSYLDPIPLKXLRVKGXKRIIDILNKFDPVVERVIKRRXI 240
QY 255 VRRRXNGEXXGEXSGVXLDITLLEFADEDETEIKTKXXIXGLVVDXFSAGDSTAXTE 314
DB 241 VRRRXNGEXXGEXSGVXLDITLLEFADEDETEIKTKXXIXGLVVDXFSAGDSTAXTE 300
QY 315 MALAELINNPXYLXXAREEXYSVVGKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPVYKR 374
DB 301 MALAELINNPXYLXXAREEXYSVVGKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPVYKR 360
QY 375 KCXECXINGXVYPGALXXFNVMQVGDXXKYWRDPSXRPFLFYTAEGEAXXLDLRG 434
DB 361 KCTEBCINGXVYPGALXXFNVMQVGDXXKYWRDPSXRPFLFYTAEGEAXXLDLRG 420
QY 435 XHFQLLPFGSGRMCVGYLATSXATLASLIQCFLDQVLPQOQIILKGADAKVSMER 494
DB 421 QHFQLLPFGSGRMCVGYLATSXATLASLIQCFLDQVLPQOQIILKGADAKVSMER 480
QY 495 AGLTVPRAHSIVCVPLARIG 514
DB 481 AGLTVPRAHSIVCVPLARIG 500
```

```
RESULT 14
US-10-732-923-1101
Sequence 1101, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgeton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 1101
LENGTH: 500
TYPE: PRT
ORGANISM: Medicago sativa
US-10-732-923-1101
```

```
Query Match          91.0%; Score 2173; DB 5; Length 500;
```

```
Best Local Similarity 86.4%; Pred. No. 4,8e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
```

```
QY 15 FxHLRPTPYAXSKALRHLNPNPSPXPRLPFIIGHXHLKDKLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTPYAXSKALRHLNPNPSPXPRLPFIIGHXHLKDKLHYAXIDLKSKHGPLFSLY 60
QY 75 FGSMPVAVASTPELFLFLQTHXATSFYTRFQTSAXRKLTYDXVAXXPXGPMXKFRKL 134
DB 61 FGSMPVAVASTPELFLFLQTHXATSFYTRFQTSAXRKLTYDXVAXXPXGPMXKFRKL 120
QY 135 IMNDLXNATTVNXXLRPLRTQOIRKXLRMAOXAAXKPLDYTELLKMNSTXSMXKIGE 194
DB 121 IMNDLXNATTVNXXLRPLRTQOIRKXLRMAOXAAXKPLDYTELLKMNSTXSMXKIGE 180
QY 195 ABEIRDIAREVLKIXGEYSYLDPIPLKXLRVKGXKRIIDILNKFDPVVERVIKRRXI 254
DB 181 ABEIRDIAREVLKIXGEYSYLDPIPLKXLRVKGXKRIIDILNKFDPVVERVIKRRXI 240
QY 255 VRRRXNGEXXGEXSGVXLDITLLEFADEDETEIKTKXXIXGLVVDXFSAGDSTAXTE 314
DB 241 VRRRXNGEXXGEXSGVXLDITLLEFADEDETEIKTKXXIXGLVVDXFSAGDSTAXTE 300
QY 315 MALAELINNPXYLXXAREEXYSVVGKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPVYKR 374
DB 301 MALAELINNPXYLXXAREEXYSVVGKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPVYKR 360
QY 375 KCXECXINGXVYPGALXXFNVMQVGDXXKYWRDPSXRPFLFYTAEGEAXXLDLRG 434
DB 361 KCTEBCINGXVYPGALXXFNVMQVGDXXKYWRDPSXRPFLFYTAEGEAXXLDLRG 420
QY 435 XHFQLLPFGSGRMCVGYLATSXATLASLIQCFLDQVLPQOQIILKGADAKVSMER 494
DB 421 QHFQLLPFGSGRMCVGYLATSXATLASLIQCFLDQVLPQOQIILKGADAKVSMER 480
QY 495 AGLTVPRAHSIVCVPLARIG 514
DB 481 AGLTVPRAHSIVCVPLARIG 500
```

```
RESULT 15
US-10-732-923-24071
Sequence 24071, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgeton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 24071
LENGTH: 500
TYPE: PRT
ORGANISM: Lens culinaris
US-10-732-923-24071
```

```
Query Match          91.0%; Score 2173; DB 5; Length 500;
Best Local Similarity 86.4%; Pred. No. 4,8e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
```

```
QY 15 FxHLRPTPYAXSKALRHLNPNPSPXPRLPFIIGHXHLKDKLHYAXIDLKSKHGPLFSXX 74
DB 1 FLHLRPTPYAXSKALRHLNPNPSPXPRLPFIIGHXHLKDKLHYAXIDLKSKHGPLFSLY 60
QY 75 FGSMPVAVASTPELFLFLQTHXATSFYTRFQTSAXRKLTYDXVAXXPXGPMXKFRKL 134
DB 61 FGSMPVAVASTPELFLFLQTHXATSFYTRFQTSAXRKLTYDXVAXXPXGPMXKFRKL 120
QY 135 IMNDLXNATTVNXXLRPLRTQOIRKXLRMAOXAAXKPLDYTELLKMNSTXSMXKIGE 194
DB 121 IMNDLXNATTVNXXLRPLRTQOIRKXLRMAOXAAXKPLDYTELLKMNSTXSMXKIGE 180
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Db	121	LMNDLNAATTWKLPLRQOIRKFLRWVAQSAEAKPLDVTYBEILKMTNSTISMMWLE	180
Oy	195	ABEIFDIAREVLKIXGEYSLDFPIKPKLKKQKTEKRIDDILINKDPVVERVYIKRRXI	254
Db	181	ABEIIDIRAEVLIKGEYSLDFIWLKYLKVGKEKRIDDILINKDPVVERVYIKRRREI	240
Oy	255	VRRNRGAXXEGEGVYLDTLLEFADETYEKITTCKXIXGLVYXPSAGXDSCTXTE	314
Db	241	VRRNRGEVVEGEAGVPLDTLLEFADETMEIKITKEQIKGLVVPFSAIGDSTVATE	300
Oy	315	WALAEILNNPYLXXAREEYSVGKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPVYKR	374
Db	301	WALAEILNNPKLQKAREEYSVGKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPVYKR	360
Oy	375	KCXEECXINGVXPBGALXXFNWVGKDXKYWRDPSERKPERFLETXAGEAXXLDLNG	434
Db	361	KCTECEINGHVIPGALVLFNWWQGRDPKYWRDPSERPERFLETXAGEAGPLDLRG	420
Oy	435	XHFOLLPRGSGAXMCPGYVLATISGAXTLLASLIQCEDLVLFGRGQGLKGDAXKSMERR	494
Db	421	OHFOLLPRGSGRMCPGVNLATISGMATLLASLIQCEDLVLFGRGQGLKGDAXKSMERR	480
Oy	495	AGLTVBRAHSLVCVPLARIG 514	
Db	481	AGLTVBRAHSLVCVPLARIG 500	

Search completed: December 22, 2005, 00:15:11
Job time : 116 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 22, 2005, 00:15:20 ; Search time 283 Seconds
(without alignments)
955.390 Million cell updates/sec

Title: US-09-857-581b-66

Sequence: 1 MLELALGXVLAFLXHLRP.....ASHIVCPARIAGVSKLIS 521

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0	Ygapext 0.5	
Delop 6.0	Delext 7.0	

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-Q=/cg21_1/USPRO.spool_p/US09857581/runat_15122005_083138_19467/app_query.fasta.1.711
-DB=published Applications NA New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCT=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62
-TRN=human40.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09857581_@CGN_1_1_183_@runat_15122005_083138_19467
-NCPU=6 -ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications NA New:
1: /cg21_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cg21_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cg21_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cg21_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cg21_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cg21_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cg21_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cg21_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
9: /cg21_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cg21_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	398	16.7	1690	6	US-10-667-295-204
2	387.5	16.2	1799	6	US-10-667-295-138
3	381.5	16.0	1794	6	US-10-667-295-80
4	240.5	10.1	1509	6	US-10-821-234-702
5	228.5	9.5	2623	6	US-10-131-826A-63
6	225	9.4	3295	7	US-11-112-908-17
7	191	8.0	1676	7	US-11-102-240-53
8	190	8.0	1710	7	US-11-000-463-641

9	190	8.0	1710	7	US-11-000-463-642	Sequence 642, App
10	190	8.0	1710	7	US-11-000-463-643	Sequence 643, App
11	187	7.8	1806	6	US-11-000-463-169	Sequence 169, App
12	186.5	7.8	1473	6	US-10-507-106-1	Sequence 1, App1
13	183	7.7	1882	7	US-11-000-463-170	Sequence 170, App
14	181	7.6	1685	6	US-10-957-569-27	Sequence 27, App1
15	180	7.5	2361	6	US-10-995-561-81	Sequence 81, App1
16	176	7.4	2361	6	US-10-995-561-80	Sequence 80, App1
17	176	7.4	2361	6	US-10-995-561-82	Sequence 82, App1
18	175.5	7.3	1547	7	US-11-000-463-171	Sequence 171, App
19	161.5	6.8	1512	6	US-10-821-234-675	Sequence 675, App
20	158	6.6	1934	6	US-10-507-106-3	Sequence 3, App1
21	157	6.6	2243	6	US-10-131-826A-107	Sequence 107, App
22	150.5	6.3	1657	7	US-11-186-284-225	Sequence 225, App
23	142.5	6.0	1566	6	US-10-821-234-694	Sequence 694, App
24	124	5.2	95223	7	US-11-117-187-188	Sequence 188, App1
25	102.5	4.3	452	6	US-10-667-295-38	Sequence 38, App1
26	99	4.1	14172	7	US-11-075-185-2	Sequence 2, App1
27	97.5	4.1	1221	7	US-11-075-185-53	Sequence 53, App1
28	97.5	4.1	31973	6	US-10-995-561-13229	Sequence 13229, A
29	89	3.7	1452	7	US-11-112-908-284	Sequence 284, App
30	89	3.7	14911	7	US-11-112-908-63	Sequence 63, App1
31	89	3.7	157230	7	US-11-112-908-64	Sequence 64, App1
32	89	3.7	170508	7	US-11-112-908-65	Sequence 65, App1
33	89	3.7	173115	7	US-11-112-908-65	Sequence 65, App1
34	84.5	3.5	761	6	US-10-497-135-18	Sequence 18, App1
35	82.5	3.3	767	6	US-10-497-135-17	Sequence 17, App1
36	78	3.3	116856	7	US-11-143-980-1	Sequence 1, App1
37	77.5	3.2	530	7	US-11-072-510-6	Sequence 6, App1
38	77	3.2	1534	6	US-10-750-185-38375	Sequence 38375, A
39	77	3.2	60486	6	US-10-995-561-13310	Sequence 13310, A
40	76.5	3.2	1719	6	US-10-750-185-61006	Sequence 61006, A
41	76	3.2	1917	7	US-11-055-822-819	Sequence 819, App
42	76	3.2	2512	6	US-10-750-185-49783	Sequence 49783, A
43	75	3.2	191684	7	US-11-121-086-2	Sequence 2, App1
44	75	3.1	187745	7	US-11-121-086-83	Sequence 83, App1
45	74.5	3.1	167891	7	US-11-121-086-14	Sequence 14, App1

ALIGNMENTS

RESULT 1
US-10-667-295-204
; Sequence 204, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OR INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411, 823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 1690
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1690)
; OTHER INFORMATION: Ceres Seq. ID no. 12450440
US-10-667-295-204

Alignment Scores:
Pred. No.: 4.18e-43 Length: 1690
Score: 398.00 Matches: 136
Percent Similarity: 42.51% Conservative: 77
Best local Similarity: 27.15% Mismatches: 226
Query Match: 16.66% Indels: 63
DB: 6 Gaps: 18

[illegible]

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QY      373  LysArgLysCys***GluGluCys***IleasnGly****Val***ProGluGluValAlaLeu 392
Db      1223  CCGCAGCATGAACCTCGAGAGAGCGCAAGCTCGCGGCTACACCATCCCAAGGAGCTTCAG 128
QY      393  ****PheAsnValTTPrgInValGly***Asp***LysTyrTTPAsparProSergLiu 412
Db      1293  GTGGGTGTCACACGCTGTGTGGCTGGCCCAACAATCCGAGAGCTGTGGGACAAGCCGAGAG 134
QY      413  **ArgProGluArgPheLeuGluThr**AlaGluGlyGluAla*****IeuAspLeu 432
Db      1343  TTTCGGCCGAGAGCGGTCTCTA-----GGCGAGAGAGAGACGCTGGACGCGC 138
QY      433  Arg-----Gly**HisPheGlnIleuProPheGlySergLysArg**MetCys 449
Db      1398  ACCGTGGCGGAGAGAGTGAAGTCTCCGCTTCCTCGCGCTTCGGCGTGGCGCGCGAGCTGC 144
QY      450  ProGluVal**LeuAlaThrSergLys**AlaThrLeuLeuAlaSerIeuLeuGlnCys 469
Db      1448  CCGGGATCATCTCTCGCCCTGCGCCATCCCGGCGTCATGTCGGCAAGCTCGCGGACAG 150
QY      470  PheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly**AspAlaLysVal 489
Db      1508  TTCAGATAGGT-ACCACCGCGCGCGGTGGAGAA----- 153
QY      490  SerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerIeuValCysValPro 509
Db      1540  GCTCAGCTCAGCGAGAAAGAGACAGATTTCAGCTGCACAT-----TGCACACCA 159
QY      510  Leu 510
Db      1591  CTC 1593

RESULT 2
US-10-667-295-138
; Sequence 138, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascoia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Glycine max
; NAME/KEY: misc_feature
; LOCATION: (1)...(1799)
; OTHER INFORMATION: Ceres Seq. ID no. 13531805
US-10-667-295-138

Alignment Scores:
Pred. No.:      1,236-41      Length:      1799
Score:          387.50      Matches:      135
Percent Similarity: 40.78%      Conservative: 73
Best Local Similarity: 26.47%      Mismatches:  227
Query Match:     16.22%      Indels:      75
DBs:            6          Gaps:         15

US-09-857-581B-66 (1-521) x US-10-667-295-138 (1-1799)
QY      35  ProProSerPro**ProArgLeuProPheIleGlyHis**HisIleuLeuLysAspLys 54
Db      162  CCACCGGGGCCCACTCCCC---GTCGCAATCTTCGGCAACTGGGCTCCAGTCCGAGCGAGAC 218
QY      55  LeuLeuHisTyrAla***IleAspLeuSerLysLysGlyProLeuPheSer***** 74

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Db      219 CTCACACCGCAACCTCAACGATTGGCCAAAATTCGGTGACATCTTCTCTCCG 278
Qy      75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLeuGln 94
Db      279 ATGGGACAGCGCAACCTCGTCGTGTTCTTCCCTGAGCTCCCAAGAGGTTCTCCAC 338
Qy      95 ****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db      339 ---ACCGAGGCGGTGAGTTCCGCTCCGC-----ACCGCAACGTCGTC 380
Qy      115 TyrAsp-----*****ValAla*****Pro***GlyProTyrTrp 128
Db      381 TTCGACATCTTCAACCGAAAGGCCAAGACATGCTTTCACCGCTCAACGCGGACATCG 440
Qy      129 ***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***Leu 148
Db      441 CGCAAAATGCGCGCATCATG-----ACCGTCCCTCTTCTC 476
Qy      149 ArgProLeuArgThrGlnGlnIleArg----- 157
Db      477 ACCAACAGGTGTGCAACAATACCGCATGATGGGAATCGAGAGCTGCGCGCTGTC 536
Qy      158 Lys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGlu 177
Db      537 GAGGACGTCAAGAAAACCCCGACGCGCGCTCCGCGCACCGTCATCCGCGCGCTT 596
Qy      178 GluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGlu 197
Db      597 CAGCTCATGATGTACCAACATGATACCGCATATATATTCACCGAGGTTTCGAGGCGG 656
Qy      198 IleArgAspIleAlaArgGluValLeuLysIle***Gly----- 210
Db      657 GAGGATCCCATCTTCCAGAGCTTAAGACCTTGAACGAGAGAGAGTCCGTTGGCGCAG 716
Qy      211 -----GluTyrSerLeuThrAspPheIle***ProLeuLys----- 223
Db      717 AGCTTGAGTATACATGATGATTTATTCCTTGAAGACCTTCTTGAAGGCTTAC 776
Qy      224 LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProVal 243
Db      777 TTGAAGATTTGCAAGAGGTGAGAGAGAGGTTGAAGCTTTTCAAGAGATTACTTCGTT 836
Qy      244 ValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu*** 263
Db      837 GACGAGAGG-----AAGAGCTTGAAGACCAAGAGCAACCAACAAATATGA--- 887
Qy      264 ***GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGlu 283
Db      888 -----CTTAATGCGCTATTGACCAATTTTGATGCC 920
Qy      284 Thr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSer 303
Db      921 CAGAGAAAAGCGGATCAACAGAACACACGCTCTTACATGTTGAAAACATCAACGTT 980
Qy      304 AlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsn 323
Db      981 GCTGCAATTGAAACAATCTATGTCGATGTAGTGGGCAATTCCTGAGCTTGTGAACAC 1040
Qy      324 Pro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***Leu 343
Db      1041 CCAGAGATCCAGCAAAAGTTAAGGATGAGATTGACAGAGTTCTTGGAGCGAGCACCA 1100
Qy      344 ValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPhe 363
Db      1101 GTGACTGACGAGACATCCAAAGCTCCATCTTCCACAGCAGTGTCAAGGAACTCTT 1160
Qy      364 ArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys***Ile 382
Db      1161 CGTCTTAAGATGGCAATCCCTCTCTTGTACACACATGAACCTCCAGACGCAAAAGCTT 1220
Qy      383 AsnGly***Val***ProGluGlyValLeu*****PheAsnValTrpGlnValGly*** 402
Db      1221 GGGGGCTATGATATCCAGCTGAGAGCAAGATCTTGATGATGATGATGATGATGATG 1280

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Qy      403 Asp***LysTyrTyrAspArgProSerGlu***ArgProGluArgPheLeuGlnThr 422
Db      1281 AACCTGCACACCTGGAAGAGCCAGAGAGTTCCGCGCTGGAAGGTTCTTTCAG----- 1334
Qy      423 AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPhe 442
Db      1335 -----GAGAGTCTGCTTGTGAAGCCAAATGGCAATGACATTAGTACCTTCCCTT 1385
Qy      443 GlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeu 462
Db      1386 GGTGTGGAGAGAAAGAGCTCCCTGGAATCATCTTTCGATTCGCAATTCCTGGCATCAT 1445
Qy      463 LeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeu 482
Db      1446 TTGGAGAGTTGGTCCAAACTTTCAGCTC-----TTCCCTCCCTCCGCGCAG----- 1493
Qy      483 LysGly***AspAlaLysValSerMetGluGluArgAlaGly-----LeuThrVal 499
Db      1494 -----TCACAGATGACACTAGTGAAGAGAGGCAATTTAGCTTGCACATA 1541
Qy      500 ProArgAlaHisSerLeuValCysValPro 509
Db      1542 CTCACGATTCACCACTTGTGGCAAGCCA 1571

RESULT 3
US-10-667-295-80
; Sequence 80, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1794)
; OTHER INFORMATION: Ceres Seq. ID no. 12558789
US-10-667-295-80

Alignment Scores:
Pred. No.:      8e-41      Length:      1794
Score:          381.50      Matches:      137
Percent Similarity: 41.79%      Conservative: 82
Best Local Similarity: 26.15%      Mismatches: 236
Query Match:      15.97%      Indels:      69
DB:              6        Gaps:      19

US-09-857-581b-66 (1-521) x US-10-667-295-80 (1-1794)
Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db      97 CTCTTGTCTGGAGAGTCTT-----ATCCCGCTCTTCGTGGCGGTATCTC 144
Qy      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
Db      145 GCCACGATGATTGAAGAGCTCCGCGCAGAGAAATTTGAAGTACCTCCAGGTCCTATGACA 204
Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
Db      205 ---ATTCGATCTTCGGAACCTGGCTTCAAGTCCGAGATGATCTCAACACCGTAATCTC 261
Qy      61 IleAspLeuSerLysLysGlyProLeuPheSer*****PheGlySerMetProThr 80

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Db      262  GTCCGATTACCGCTAAGAAATTCGGCGATCTCTCTCCGTATGGGTACGAAACCTA 321
Qy      81  ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
Db      322  GTCCGTGCTCCCTCCACCGGATCTTAACAAGAAAGTGCTC---CTCACTCAAGCGTTGAG 378
Qy      101  Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrArgPhe***** 116
Db      379  TTTGGATCCAGA-----ACGAGAAAGCTGCTGTTCGACATTTCACCCGGG 423
Qy      117  *****ValAla*****Pro**GlyProTyrTrp**PheValArgLysLeu 134
Db      424  AAGGTCACAGATATGGTGTTCACCTGTACGCGAGCATTTGAGAGAAATGAGAAATC 483
Qy      135  IleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGln 154
Db      484  ATG-----ACGGTTCCTTTCTTCAACCAACAAAGTTGTTCAA 519
Qy      155  GlnIleArgLys**LeuArg*****MetAlaGln**AlaGluAla**Lys----- 171
Db      520  CAGAAATCGTACAGCTTGGGAGTTTGAAGCAGCTAAGTGTGTAAGATGTTAAGAAAT 579
Qy      172  ProLeuAsp**ThrGlu-----GluLeuLeuLysTrp** 183
Db      580  CCGAATTCGTCTCGTACGAAAGAAATCGTGTGAGGAAACGTTTGAATGATGATATAC 639
Qy      184  AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgPheIleArg 203
Db      640  AATATGTTCCGTATCATGTTGATAGAAAGATTTGAGAGTATGATCTCTTTTCCTT 699
Qy      204  GluValLeuLysIle**Gly-----GluTyrSerLeu 214
Db      700  AGCGTTAAGCCTTGAATGATGTGAGAGAAATCGATTAGCTCAGACCTTGGATTAATAT 759
Qy      215  ThrAspPheIle**ProLeuLys**LeuLysValGlyLysTyrGluLysArgLysLeu 234
Db      760  GGAGATTTTCATCTCTTACCTTACCTTACGACCATTCCTCAGAGGC---TATTTGAAGATTTGCA 816
Qy      235  AspIleLeuAsnLysPheAspProValValGluArg---ValIleLysLysArgArg** 253
Db      817  GATGTGAAAGATCGAAGAAATCGCTCTTTTCAAGAGATCTTGTGTGAGAGAGAAACA 876
Qy      254  IleValArgArgArg**AenGlyGlu*****GluGlyGlu**SerGlyVal**Leu 273
Db      877  ATTGCCAGTCTTAAGCTTACAGGT-----AGTAAAGATGAAATGCGCAT 924
Qy      274  AspThrLeuLeuGluPheAlaGluAspGluThr**GluIleLysIleThrLys***** 293
Db      925  GATCAGCATCTCTGAA---GCTGAGCAGAGAGGA-----GAAATCAACGAGACAAAT 972
Qy      294  Ile***GlyLeuValValAsp***PheSerAlaGly**AspSerThrAla*****Thr 313
Db      973  GTTCTTTACATCGTCGAGAACATCAATGTGCGCCGATTTAGACAAACATTTGGTCTATC 1032
Qy      314  GluThrAlaLeuAlaGluLeuIleAsnAsnPro**ValLeu*****AlaArgGluGlu 333
Db      1033  GAATGGGGAATTTGACAGCTAGTGAACCATCTCAAAATCCAGAGTAACTTAAGAGACGA 1092
Qy      334  **TyrSerValValGlyLysAsp**LeuValAspGluValAspThrGlnAsnLeuPro 353
Db      1093  CTCGACACAGTTCCTTGACCGGGGTGTCAGATCACAGCGCTGATCTTCAAAACCTTCCA 1152
Qy      354  TyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuPro---ValVal 372
Db      1153  TACCTTCAAGCTGTGTTAAGAGACATCTTCGTCTGAAATGCGGATTCCTCTCTGCTG 1212
Qy      373  LysArgLysCys**GluGluCys**IleAsnGly**Val**ProGluGlyAlaLeu 392
Db      1213  CCTCACATGAACCTCCATGATGCGAAGCTGCTGGCTACATATCCACGAAAGACAA 1272
Qy      393  ****PheAsnValTyrGlnValGly**Asp**LysTyrTyrAspArgProSerGlu 412
Db      1273  ATCTTGTATATGCTGTGTGCTGCTAGCAAAACACCCCAACAGCTGGAAGACCTGAGAG 1332

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Qy      413  ***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeu 432
Db      1333  TTTAGCCAGAGAGGTTCTTTGAA-----GAAAGATCGACGTGAAAGCT 1377
Qy      433  ArgGly**HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal 452
Db      1378  AACGGTAAATGACTTACAGGTATATGGCATTTGGGTGTGAGCGTGAAGCTGCCGGGATT 1437
Qy      453  ***LeuAlaThrSerGly**AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeu 472
Db      1438  AATATGGCAATTCCTATTTTGGGAGATCAACCATTTGGATGAGATGTCGAAACTTCAGCT 1497
Qy      473  GlnValLeuGlyProGlnIleGlnIleLeuLysGly**AspAlaLysValSerMetGlu 492
Db      1498  -----CTTCCTCTCTCAGAGCAG-----TCTAAATGATACTACT 1533
Qy      493  GluArgAlaGly 496
Db      1534  GAGAAAGCTGGA 1545

RESULT 4
US-10-821-234-702
; Sequence 702, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stachne-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 702
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-702

Alignment Scores:
Pred. No.: 9,21e-22 Length: 1509
Score: 240.50 Matches: 120
Percent Similarity: 37.80% Conservative: 83
Best Local Similarity: 22.35% Mismatches: 261
Query Match: 10.07% Indels: 73
DB: 6 Gaps: 20

US-09-857-581b-66 (1-521) x US-10-821-234-702 (1-1509)
Qy      6  AlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro----- 22
Db      10  GCGATGGGCTCTGTGGCGGGGTGCGCTCGGAGAGGTGCATCTCGAATCTCTCACTG 69
Qy      23  -----***Ala***SerLysAlaLeuArgHisLeuProAsn----- 34
Db      70  GGCATGTGCGCTTCTGTCTGCTGCTGCTGCTTCTTCAAAAGCGGCGCCCAAGAACTAC 129
Qy      35  ProProSerPro**ProArgLeuProPheIleGlyHis***HisLeuLysAspLys 54
Db      130  CGCGCGGGGCGCTGG---CGCTGCGCTTCTTGGCAACTTCTTCTGTGAGACTTGCAG 186
Qy      55  LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db      187  CAGTCGCACTGGAAGGTTGACGCTGTTGTGAAGAAATATAGGGAACCTTTTACCTTGAG 246
Qy      75  PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db      247  CTGGTGACATATATCTCAGATCTTATTAAGCTTCCCTTAATCAAAAGAACCTTATTC 306

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Score:	226.50	Matches:	118
Percent Similarity:	38.97%	Conservative:	78
Best Local Similarity:	23.46%	Mismatches:	230
Query Match:	9.46%	Indels:	77
DB:	6	Gaps:	21

US-09-857-581B-66 (1-521) x US-10-131-826A-63 (1-2623)

QY 1 MetLeuGluLeuAlaLeuGlyLeu***Val---LeuAlaLeuPhe***HisLeuArg 19
 Db 65 CTGCTGCTGCGCTGGCGCTGCTCTGCTGCTGACGCTGGCGCTG----- 1099
 QY 20 ProThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProProSerPro*** 39
 Db 110 -----TCCGGAGACCAAGGGCCGACACTG-----CCCCCGGGCCACG 151
 QY 40 ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisIleTyrAla 59
 Db 152 CCG---CTACCACTGCGGAAACCTCTGCACACTACGCGCGGCGCTGTTATTCAGG 208
 QY 60 ***IleAspLysSerLysLysHisGlyProLeuPheSer*****PheGlySer---Met 78
 Db 209 CTCATGCGCGCTGAGTATGAAAGTACGAGACCGGTGTTCACATCTACCTGGGACCTGGCGG 268
 QY 79 ProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAla 98
 Db 269 CCTGTGCTGTCTCTGTGGTGGCGAGAGGCTGTGCGGAGGCGCTG---GGAGGTACAGCT 325
 QY 99 ThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp***** 118
 Db 326 GAGGACTTCAGCGCGCGG---GGAGACCGTAGCATGTGTGAGAGGAGACTTGTGTGGCCAT 382
 QY 119 ValAla*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAsp 138
 Db 383 GGGGTTTCTTCTCCACCGGGAGCGGTGAGGACGACTGAGAGATT----- 430
 QY 139 Leu***AsnAlaThrThrValAsn***LeuArgProLeu-----Arg 152
 Db 431 -----ACCATGCTTGTCTGCGGACTGTGGGACTGTGGGAGCGAGAGAGC 475
 QY 153 ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***** 170
 Db 476 GAGGACCTGATCCAGGCGGAGCGCGCGGTGCTGTGTGAGACATTCCAGGGGACAGAGA 535
 QY 171 LysProLeuAsp***ThrGluGluLeuLysTrp***AsnSerThr***SerMetMet 190
 Db 536 CGCCCACTTGATCCCTCCCTGCTGCTGCGCCACGACCTCCACAGTATCTGCTCCCTC 595
 QY 191 ***LeuGly-----GluAlaGluGluIleArgAspIleAlaArg----- 203
 Db 596 CTCTTGGCTCGCTTCCTTCATAGAGATAGAGATGATTCAGAGCGCGGTGCGGAGACT 655
 QY 204 -----GluValLeuLysIle***GlyGlu-----TyrSerLeuThrAsp-- 216
 Db 656 GGTGTACCTCGCTGGAGATCACTCCACAGGGGGGTGCAGCTACGAGATGTTCTCTGG 715
 QY 217 PheIle***ProLeuLys***LeuLysValGlyLysTrpGluLysArgIleAspAspIle 236
 Db 716 TTCTCTGCGGCGCTTGCCA-----GGCCCCACAGACGACTCTCCACACACTC 763
 QY 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
 Db 764 AGCAGCTTGAGCTGCTTCACAGATCCGGCAGGTGAGAGACAGACAGGGGAGACTG----- 817
 QY 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThr-- 275
 Db 818 -----GATGCTTCGGGAGCCCGCCGACGTGACTGTC 847
 QY 276 -----LeuLeuGluPheAlaGluAspGluThr***Glu---IleLysIleThrLys 291
 Db 848 GATGCTTCTGCTGTTGAAGATGACACAGGAGAGACAAACCAGGACACAGATTCACCAAC 907
 QY 292 *****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*** 311

Db	908	AAGAAACATGCTGAAAGCAGTCATATTATTGCTGTTGCTGGAGACGATGACGGTACAGCC	967
Qy	312	**ThrgIuTPAlaLeuAlaGluLeuIleAsnAsnPro**ValIleu*****AlaArg	331
Db	968	ACGGTCGGCTATACCCCTCCTGCTCTGATGAAATATACCTCATGTCCAAAGATGGGTACGT	1027
Qy	332	GLUGlu**YrSerValValGlyLysAsp**LeuValAspGluValAspThrGlnAsn	351
Db	1028	GAGGAGCTGAATCGGAGCTGGGGGCTGGCCAGGACCAAGCTTAGGGGACCGTACCCGC	1087
Qy	352	LeuProTYrIleArgAlaIleValIleGluThrPheArgMetHisProProLeuProVal	371
Db	1088	CTCCCTTATACCGACGGCGTTCTCATGAGGCGCAGCGGCTGCTGGCGCTGTGCCATG	1147
Qy	372	--ValIysArgLysCys**GluGluCys**IleAsnGly**Val**ProGluGly	390
Db	1148	GGAATATACCCGACCCCTCATGCGGACCAACCCGCTTCGAGAGGTACACCTGCCACAGGC	1207
Qy	391	AlaIleu*****PheAsnValTTPGlnValGly**Asp**LysYrTTPAspArgPro	410
Db	1208	ACGGAGGTCTTCCCTCCTTGGCTGCATCTCGATACCCCAATCTTAAAGCACCCA	1267
Qy	411	SerGlu**ArgProGluArgPheLeuGluThr**AlaGluGlyGluAla*****Leu	430
Db	1268	GAAAGTTCAACCAACGACGTTCTTGAT-----GCAATGAGACGTTACG-----	1315
Qy	431	AspleuArgGly**HisPheGlnLeuLeuProPheGlySerGlyArg**MetCysPro	450
Db	1316	-----AAGCATGAGAGCGCTCCCTGCTTCTTACGGAAGCGTGTGCCTT	1363
Qy	451	GlyVal**LeuAlaThrSerGly**AlaThrLeuLeuAlaSerLeuIleGlnCysPhe	470
Db	1364	GAGAGGCGCTCGGCAAAAGCGACCTTTCCTCTTCAACCAACATCTTCAAGCCCTTC	1423
Qy	471	AspleuGln 473	
Db	1424	TCCCTGGAG 1432	
RESULT 6			
US-11-112-908-17			
; Sequence 17, Application US/11112908			
; Publication No. US20050260659A1			
; GENERAL INFORMATION:			
; APPLICANT: Harris, Lisa M.			
; TITLE OF INVENTION: Breast Cancer Biomarkers			
; FILE REFERENCE: 04-164-US			
; CURRENT APPLICATION NUMBER: US/11/112, 908			
; PRIOR FILING DATE: 2005-04-22			
; PRIOR APPLICATION NUMBER: US 60/564, 758			
; PRIOR FILING DATE: 2004-04-23			
; PRIOR APPLICATION NUMBER: US 60/575, 978			
; PRIOR FILING DATE: 2004-06-01			
; PRIOR APPLICATION NUMBER: US 60/631, 702			
; PRIOR FILING DATE: 2004-11-30			
; PRIOR APPLICATION NUMBER: US 60/633, 826			
; PRIOR FILING DATE: 2004-12-07			
; NUMBER OF SEQ ID NOS: 511			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 17			
; LENGTH: 3295			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-112-908-17			
Alignment Scores:			
Pred. No.: 3,74e-19			
Score: 225.00			
Percent Similarity: 36.11%			
Best Local Similarity: 20.42%			
Query Match: 9.42%			
DB: 7			
Gaps: 16			

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US-09-857-581b-66 (1-521) x US-11-112-908-17 (1-3295)
QY 32 LeuProAsnProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeu 51
DB 578 CTGCCCGGGCCCAACGAC-----TGGCAGCTGCTGGGC-----AGCCTGCTG 619
QY 52 LysAsp-----LysLeuLeuHisTyrAla***IleAspLeuSerLys 65
DB 620 CAATCTCTCGAAGAGGGGCTCCAGAAACAGACAGACCCGTGGAGTACCAAG 679
QY 66 LysHisGlyProLeuPheSer****PheGlySerLeuProThrValAlaIleSerThr 85
DB 680 AAGTATGGCAAGATTTTCCGATGAAAGTTGGGTTCTTTGATCGGAGCCTCGGCTCG 739
QY 86 ProGluLeuPheLysLeuPheLeuGln****GluAlaThrSerPhe***ThrArgPhe 105
DB 740 CCATGCTCTGGAAGGCTGTACCGCAGAGCGCG----- 778
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp****ValAla*****Pro***Gly 125
DB 779 -----TACCCGAGCGGCTGGAGATCAACCGTGAAG 811
QY 126 ProTyrTrp***PheValArgLys-----LeuIleMetAsnAspLeu***AsnAla 142
DB 812 GCCATCGCGACTACCGCAAGAGGCTACGGGCTGCTGATC----- 853
QY 143 ThrThrValAsn***LeuArgProLeuArgThrGlnIleLeuArgLys***LeuArg*** 162
DB 854 -----CTGGAAAGGGGAGACTGCGAGCGGGCTCGAGTGCCTTTCAA-- 895
QY 163 MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLysTrp 182
DB 896 -----AAGAACTAATGAAACAGAGGGAAGTATGAAGCTG 931
QY 183 ***AsnSerThr***SerMetMet***-----LeuGlyGluAlaGluGlnIleArgAsp 200
DB 932 GACACAAATTCATAGAGTCTTGCGCATTTTATGGAGAAATGATGAGCTCTGAT 991
QY 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
DB 992 GAAAGAGCGCACGTCGAAGACTTGTACAGCACTGAAACAAATGTCGTTT----- 1042
QY 221 LeuLys***LeuLysValGlyLysLeuLysArgLys----- 233
DB 1043 ---GAAAGTATCTGCTCGCTGTGTATGAGAAAGATTTGGGCTTTCAGAGAAATGCA 1099
QY 234 ---AspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg 252
DB 1100 GGGGATGAAGCTGGAAGTTCATCATGAGCCATCAAAACATGATGAGAGCTTTGGAGG 1159
QY 253 ***IleVal-----ArgArgArg***AsnGlyGlu*****GluGlyGlu 267
DB 1160 ATGATGTCACCTCAGTCAGAGCTCAGCAAGAGCTCAACAGAGTCTGCGAGAGCAC 1219
QY 268 ***SerGlyVal***LeuAspThrLeuLeu----- 277
DB 1220 ACT-----CTGGCCTGGGACACATTTTCAATCATGCTCAAGCTTGTATGACACCGG 1273
QY 278 -----GluPheAlaGluAspGluThr**GluIle 287
DB 1274 TTAGAAGAGTATTCACGACAGCTAGTCAGATTTCTTTGTGACATTATCACAGAT 1333
QY 288 LysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly***Asp 307
DB 1334 CGGCTTTCAGAGGAAGATGTATGCTCTGTCACAGAGCTCCAGCTGGCGGTGAA 1393
QY 308 SerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAspPro***ValLeu 327
DB 1394 ACGACAGCAAAACAGCTATATGTGATTTCTTCAATTTTATCCCGTAATCCCAAGTCAA 1453
QY 328 *****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluVal 347

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DB 1454 CAAAGCTTCTTAGGAATTCAGATGATTAACCTGAGAAATCAGTGCCAGGCGAGAA 1513
QY 348 AspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisPro 367
DB 1514 GATTGAGGAATATATGCCGTAATTAAGAGCTCTCGAAGAAATCTATAGAGCTTACGCCG 1573
QY 368 ProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val*** 387
DB 1574 AGTGTACCAATTTTACCACTCGAGCTCTTGACAGGCAACAGTTCTGGTGAATATGCTTTA 1633
QY 388 ProGluGluValAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrp 407
DB 1634 CCCAAGGAACAGTGTCTATGCTAAATACCCAGCTTGGATTCAGTGAAGCAATTTT 1693
QY 408 AspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla 427
DB 1694 GAAGATTCAAGTCAGATTGATGACTGAACCTTGCTTCAG-----GAGAAGAA-- 1741
QY 428 *****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg*** 447
DB 1742 -----AAATTAATCCTTTGGCATCTTCCATTGCGCTTGGAAAAAGA 1786
QY 448 MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIle 467
DB 1787 ATGTGATTTGTCGCCGATTAAGCAGAGCTTCAACTGCATTGGCTCTTTGTGATTTGTC 1846
QY 468 GlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAla 487
DB 1847 CGGAATTAAGACATCCAGCGCACAGCAATGAG----- 1879
QY 488 LysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCys 507
DB 1880 -----CCTGTGAGATGCTTACACTCAAGCACCCTG 1909
QY 508 ValProLeuAlaArgIleGlyValAla 516
DB 1910 GTGCCAGCGCGGAATCCCCATGCG 1936

RESULT 7
US-11-102-240-53
? Sequence 53, Application US/11102240
? Publication No. US20050260647A1
? GENERAL INFORMATION:
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, Christopher J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Wood, William I.
? TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES
? FILE REFERENCE: P3230R1C106C
? CURRENT APPLICATION NUMBER: US/11/102,240
? PRIOR FILING DATE: 2005-04-08
? PRIOR APPLICATION NUMBER: 10/063662
? PRIOR FILING DATE: 2002-05-07
? PRIOR APPLICATION NUMBER: 10/006867
? PRIOR FILING DATE: 2001-12-06
? PRIOR APPLICATION NUMBER: PCT/US00/23328
? PRIOR FILING DATE: 2000-08-24
? PRIOR APPLICATION NUMBER: 60/170262
? PRIOR FILING DATE: 199-12-09
? NUMBER OF SEQ ID NOS: 170
? SEQ ID NO 53
? LENGTH: 1676
? TYPE: DNA
? ORGANISM: Homo Sapien
US-11-102-240-53

Alignment Scores:
Pred. No.: 5,78e-15 Length: 1676
Score: 191.00 Matches: 115
Percent Similarity: 34.03% Conservative: 63
Best Local Similarity: 21.99% Mismatches: 239

```


APPLICANT: Tang, Y Tom
 APPLICANT: Liu, Chenhua
 APPLICANT: Asundi, Vinod
 APPLICANT: Chen, Rui-hong
 APPLICANT: Qian, Xiaohong B.
 APPLICANT: Wang, Zhiwei
 APPLICANT: Wehrman, Tom
 APPLICANT: Zhang, Jie
 APPLICANT: Zhou, ping
 APPLICANT: Cao, Yi-Cheng
 APPLICANT: Dimanac, Radoje T.
 TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 FILE REFERENCE: 785CIP4CN
 CURRENT APPLICATION NUMBER: US/11/000,463
 CURRENT FILING DATE: 2004-11-29
 PRIOR APPLICATION NUMBER: 10/291,265
 PRIOR FILING DATE: 2002-11-08
 PRIOR APPLICATION NUMBER: PCT/US01/02623
 PRIOR FILING DATE: 2001-01-25
 PRIOR APPLICATION NUMBER: 09/922,279
 PRIOR FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: 09/491,404
 PRIOR FILING DATE: 2000-01-25
 PRIOR APPLICATION NUMBER: 09/617,746
 PRIOR FILING DATE: 2000-07-17
 PRIOR APPLICATION NUMBER: 09/631,451
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: 09/633,870
 PRIOR FILING DATE: 2000-09-15
 NUMBER OF SEQ ID NOS: 944
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 643
 LENGTH: 1710
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-000-463-643

Alignment Scores:
 Pred. No.: 8,15e-15 Length: 1710
 Score: 190.00 Matches: 115
 Percent Similarity: 34.03% Conservative: 63
 Best Local Similarity: 21.99% Mismatches: 239
 Query Match: 7.95% Indels: 106
 Gaps: 21

US-09-857-581b-66 (1-521) x US-11-000-463-643 (1-1710)

QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu**ValLeuAlaLeuPhe**HisLeuArgPro 20
 DB 193 CTACTCTGCTGCTGGTGGTGGCTCCTGGCTACTGCC-----CGCATCTGGCT 243
 QY 21 ThrPro**Ala**SerLySAlaLeuArgHisLeuProAsnProPheSerPro**Pro 40
 DB 244 TGGACATATGCTCTTAACAACACTGCCGCGCTCCAGTGTTCACACAGCCCCCAAA 303
 QY 41 ArgLeuProPheIleGlyHis**HisLeu-----LeuLysAsp 53
 DB 304 CGGAACGTGTTTGGGTCACTGGGCTTGATCACTCTCAAGAGAGGCTTAAAGAC 363
 QY 54 LysLeuLeuHisTyrAla**IleAspLeuSerLySHisGlyProLeuPheSer** 73
 DB 364 -----TCGACCCAGATGTCGGCCACCTATTCGAGGGCTTTACGATA 405
 QY 74 ***PheGlySer---MetProThrValAlaLaserThrProGluLeuPheLeuPhe 92
 DB 406 TGGCTGGGTCCCATCATCTCCCTCATGTTTATGACCACTGACACCATCGGTATATC 465
 QY 93 LeuGln*****GluAla-----ThSerPhe**ThrArgPheGlnThrSer 108
 DB 466 ACCAATGCTCAAGCTGCATTCACACCCAGAGATATCTCTTCATCAGGTTT----- 516
 QY 109 Ala**Arg**LeuThrTyrAsp*****ValAla*****Pro----- 123

DB 517 -----CTGAAGCCCTGCTGGAGAGGG 540
 QY 124 *****GlyProTyrTrp**PheValArgLysLeuIleMechAsnAspLeu 139
 DB 541 ATACTGCTGAGTGGGGTGAACAAGTGAAGAGCGCCACCTCGGATG-----CTG 588
 QY 140 ***AsnAlaThrThrValAsn**LeuArgProLeuArgThrGlnGlnIleArgLys*** 159
 DB 589 AGCGCCGCTTCCATTTCAACATCTGAAGTCCATATATACG---ATCTTCAACAGACT 645
 QY 160 LeuArg***MetAlaGln-----**AlaGluAla**LysProLeuAsp 174
 DB 646 GCAAAATCATATGCTTGACAAAGTGGACAGCACTGCTCAGAGGAGGAGCAAGTTGTCTGAC 705
 QY 175 ***ThrGluGluLeuLysTyr**AsnSerThr**SerMetMet**LeuGlyGlu 194
 DB 706 ATGTTTGAACATC-----AGCCTCATGACCTTGGACACT 741
 QY 195 AlaGluGlu---IleArgAspIleAlaArgGluValLeuLysIle**GlyGluTyrSer 213
 DB 742 CTACAGAAATGATCTTCAGCTTTCAGCCATTCGTACAGAGAGGCCCGCAATATATATT 801
 QY 214 LeuThrAspPheIle**ProLeuLys**LeuLysValGlyLysTyrGluLysArgIle 233
 DB 802 GCCACC-----ATCTTGAGCTCAGTGCCTT-----CTAGAGAAAGAAC 843
 QY 234 AspAspIleLeuAsnLysPheAsp----- 241
 DB 844 CAGCATATCTCCAGACATGATGACTTTCGTATTAACCTCTCCATGACGGGCGCGCTTC 903
 QY 242 -----ProValValGluArgValIleLysLysArgArg*** 253
 DB 904 CACAGGCGCTGCGCGCTGTGCATGACTTCACAGAGCTGTGATCGGAGCGGCTGCC 963
 QY 254 IleValArgArgArg**AsnGlyGlu*****GluGlyGlu**SerGlyVal**Leu 273
 DB 964 ACCCTCCCACTCAGGGATATGATGATTTTTCAAAGACAAAGCCAAATGCAAGACTTGG 1023
 QY 274 Asp-----ThrLeuLeuGluPheAlaGluAspGluThr**GluIleLysIleThrLys 291
 DB 1024 GATTTATGATGATGCTTCTGCTGACAGCAAGATGAGAGGAG---CATATGTCAGAT 1080
 QY 292 *****Ile**GlyLeuValValAsp**PheSerAlaGly**AspSerThrAla*** 311
 DB 1081 GAGCATATTAAGACAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACACAGGCGACT 1140
 QY 312 ***ThrGluThrAlaLeuAlaGluLeuIleAsnAsnPro**ValLeu*****AlaArg 331
 DB 1141 GGCCTCTCTGGGTCTGTACAACTTGGAGGACACCAATACCAAGAGCGCTGCCGA 1200
 QY 332 GluGlu**TyrSerValValGlyLysAsp**LeuValAspGluVal-----Asp 348
 DB 1201 CAGGAGGTGAAAGAGCTTCTG---AGGACCGGAGATCTTAAGATTTGAATGGAGACAC 1257
 QY 349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
 DB 1258 CTGGCCAGCTGCCCTTCTGACCATGTGGGTGAAGAGAGCTGAGTTATCATCTCCCA 1317
 QY 369 LeuProValValLysArgLysCys***GluGluCys**Ile---AsnGly***Val*** 387
 DB 1318 GCTCCCTTCATCTCCGATCTGACACGAGCAATGTTTCTTCCAGATGGCCGAGTCATC 1377
 QY 388 ProGluGluValLeuLeu*****PheAsnValTyrGlnValGly**Asp***LysTyrTrp 407
 DB 1378 CCCAAGGAGATTAACCTGCTCATCATGATATATATAGGGGTCCATGACCAACCACTGTGTGG 1437
 QY 408 AspArgProSerGlu**ArgProGluArgPheLeuGluThr**AlaGluGlyVal 427
 DB 1438 CCGATATCTGAGGTCTACGACCCCTTCCGCTTGAACCCAGAGAAACGAGAGGAGGTCA 1497
 QY 428 *****LeuAspLeuArgGly**HisPheGlnLeuLeuProPheGlySerGlyArg*** 447
 DB 1498 -----CTCTGCGCTTTATATCTTCTTCCGACGAGGCCACAG 1533

QY 448 MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuAlaSerLeuIle 467
DB 1534 AACTGATGCGGAGCGCTTGGCCATGCGGAGATGAAGAGTCTCTGGCGTTGATGCTG 1593
QY 468 GlnCysPhe 470
DB 1594 CTGCACTTC 1602
RESULT 11
US-11-000-463-169
; Sequence 169, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Jie
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radolje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIPACN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 169
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(1748)
US-11-000-463-169
Alignment Scores:
Pred. No.: 2,45e-14 Length: 1906
Score: 187.00 Matches: 113
Percent Similarity: 34.68% Conservative: 67
Best Local Similarity: 21.77% Mismatches: 241
Query Match: 7.83% Indels: 98
DB: 7 Gaps: 21
US-09-857-581B-66 (1-521) x US-11-000-463-169 (1-1906)
QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 231 CTACTCTGCTGCTGGTGTGGGCTCTGGCTACTGCC-----CCCATCTGGCT 281
QY 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
DB 282 TGGACCTATGCTTTCTATTAACAACACTGCCCGCGCTCAAGTGTTCCTCCACAGCCCCCAAAA 341
QY 41 ArgLeuProPheIleGlyHis***HisLeuLeu-----LysAspLysLeuLeuHis 57

DB 342 CGGAACGTGTTTGGGGTACCTGGGCGCTGATCACTCTACAGAGAGAGGGCTTGAAGAAC 401
QY 58 TyrAla***IleAspLeuSerLysHisGlyProLeuPheSer****PheGlySer 77
DB 402 TCGACCAAGATGTCGGCACCTATTCCAGAGC-----TTTACATATAGCTGGGTCC 455
QY 78 ---MetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln***** 96
DB 456 ATCATCCCTTCATGCTTTATGCAACCTGACACCATCCGGTCTATCAACATGCTCA 515
QY 97 GlnAla-----ThiSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
DB 516 GCTGCATTCAGACCCAGATATATCTTCATCAGGTTG----- 554
QY 113 LeuThrTyrAsp*****ValAla*****Pro----- 123
DB 555 -----CTGAAGCCCTGGCTGGAGAGAGGATACTGCTGAGT 590
QY 124 **GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThr 143
DB 591 GCGGTGACAAAGTGAAGCCGACCGCTCGGATG-----CTGACGCCCGCTTC 638
QY 144 ThrValAsn***LeuArgProLeuArgThrGlnIleArgLys***LeuArg***Met 163
DB 639 CATTCACATCCTGAAGTCTATATTAACG---ATCTTCACAAAGAGTCAAAACATCATG 695
QY 164 AlaGln-----**AlaGlnAla***LysProLeuAsp***ThrGluGlu 178
DB 696 CTGACAAATGCGACGACCTGCGCTGAGGCGACAGAGTGTCTGAGACAGTTTGAGCAC 755
QY 179 LeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGlnAlaGluGln--- 197
DB 756 ATC-----AGCTCATGACCTTGACAGCTACAGAAATGC 791
QY 198 IleArgAspIleAlaArgGluValLeuLysIle***GlyGlnTyrSerLeuThrAspPhe 217
DB 792 ATCTTCAGCTTGACAGCATTGTGACGAGAGGCGCACGAAATATATTGCCACC----- 845
QY 218 Ile***ProLeuLys***LeuLysValGlyLysTyrGlnLysArgLysAspIleLeu 237
DB 846 ATCTTGAGACTGATGCCCTT-----GTAGAGAAAAGAGCCAGCATATATCTC 893
QY 238 AsnLysPheAsp----- 241
DB 894 CAGCAATGACCTTCTGATTAACCTCTCCATGACGGGCGGCTTCACAGGGCTCG 953
QY 242 -----ProValValGluArgValIleLysLysArgArg***IleValArgArg 257
DB 954 CGCCTGTGCATGACTTCACAGACGCTGATCCGGAGCGGCTGCACCCCTCCCACT 1013
QY 258 Arg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAsp-----Thr 275
DB 1014 CAGGATATTGATGATTTTTCAAAGACCAAGCCAAAGCTTCAGACTTTTCATTTGAT 1073
QY 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
DB 1074 GTGCTTCTGTGACAGAGATGAAGTGGGAAG--GCATGTGCATGATGAGATATTAAGA 1130
QY 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTyr 315
DB 1131 GCAGAGGTGACACCTTCATGTTTGAGGCGCATGACACACGCGCAGTGGCTCTCTCG 1190
QY 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
DB 1191 GTCTCTTACAACTTTCGAGGACCCAGAAATACACAGACGCTGCGACAGAGGTGCA 1250
QY 336 SerValValGlyLysAsp***LeuValAspGluVal-----AspThrGlnAsnLeu 352
DB 1251 GAGCTTCTG--AAGAGCCGCGATCTTAAGAGATTTGAGGACACACCTGGCCCAAGCTG 1307
QY 353 ProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProValVal 372

Db 1308 CCCTTCCTGACATGTCGCGTGAAGAGACCTGAGTTACATCCCGAGCTCCCTTCATC 1367
Qy 373 LysArgLysCys***GluGluCys***Ile---AsnGly***Val***ProGluGlyAla 391
Db 1368 TCCCGAGTCGCGACCCAGCATTTGTTCTCCCAAGATGACCGAGTATCCCAAGGACATT 1427
Qy 392 Leu*****PheAsnValTpgGlnValGly***Asp***LysTyrTrpAspArgProSer 411
Db 1428 ACCTGCCTCATGATATTAAGAGGGTTCATCACACCAACTGTGTGGCCGAGATCCGTGAG 1487
Qy 412 Glu***ArgProGluArgPheLeuGluTyr***AlaGluGlyGluAla*****LeuAsp 431
Db 1488 GTCTACGACACCCCTTCGCTTTCGACCCAGAGACGCAAGGAGGAGTCA----- 1535
Qy 432 LeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGly 451
Db 1536 -----CCTGCGCTTTTATTCTCTTCCGACAGGCGCCAGAACTGCATCGAG 1583
Qy 452 Val***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuLeuGlnCysPhe 470
Db 1584 CAGCGCTTCGCCATGCGCGAGATGAAGTGTCTCTGCTGATGCTGCACTTC 1640
RESULT 12
US-10-507-106-1
; Sequence 1, Application US/10507106
; Publication No. US20050246797A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Agency
; TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
; FILE REFERENCE: 26352U (P803-31PCT)
; CURRENT APPLICATION NUMBER: US/10/507,106
; CURRENT FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-507-106-1
Alignment Scores:
Pred. No.: 1.96e-14 Length: 1473
Score: 186.50 Matches: 101
Percent Similarity: 35.81% Conservative: 77
Best Local Similarity: 20.32% Mismatches: 214
Query Match: 7.81% Indels: 105
Gaps: 17
DB: 6
US-09-857-581b-66 (1-521) x US-10-507-106-1 (1-1473)
Qy 18 LeuArgProThrPro***Ala***SerIleAlaLeuArgHisLeuProAsnProProSer 37
Db 79 CTCGATCATCTCCAGCTTCAAGAAAACTTAATGATCATCATGTATCATCCAGAGT 138
Qy 38 Pro***ProArgLeuPro----- 43
Db 139 CACGAGCAAGTTTCCACAGGAAAGCTTGGATGCGCCGTCATCGGTGAACCATGAG 198
Qy 44 PheIleGlyHis***His-----LeuLeuLysAspLysLeuLeu 56
Db 199 TTCGCTCTTCTGCTTACTCAGACCGTCCTGAGAGTTTCATGACCAACGTCGTCATG 258
Qy 57 HisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer*****PheGly 76
Db 259 -----TATGGAGAGTGTTAAGTCGCATATTTT 288
Qy 77 SerMetProThrValAlaLaserThrProGluLeuPheLysLeuGln***** 96
Db 289 GGAAGCGGAGCATGTGTGCGATGCTGAAGTGAACAGCGGTTTACAG---AGC 345
Qy 97 GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp 116
Db 346 GACTCGACAGCGTTTC---GTGCGGTTTAAACCAAAAACGTAAGGAGCTAATGGGAAA 402

Qy 117 *****ValAla*****Pro**GlyProTyrTrp***Phe-----ValArgLys 133
Db 403 TCGTCGATCTCTTATCAACCGAGATTACATGACGGTTCATGATGATGCTGCTCT 462
Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***Leu----- 148
Db 463 TTCTTAAGTCCGCACTTCTCAAGCTCAATTCGTTAGAGATGCACAAAGTTTGTGCG 522
Qy 149 -----ArgProLeuArgThrGlnIleArgLys*** 159
Db 523 GAATCATGATCTATGTCGAGAGACCAACTGTGCTCTCCAGAGACGTCACAGACT 582
Qy 160 LeuArg***MetAlaGln**AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179
Db 583 GTT-----GCATTCAAAGTACTT----- 600
Qy 180 LeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluLeuArg 199
Db 601 -----GCCAAGCATGATTAAGTGTGAGAAAGAGAAAGATTGAA 642
Qy 200 AspIleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle*** 219
Db 643 GACCTAAAGAGAGAG-----TTTGAAATTCATATCA 675
Qy 220 ProLeuLys***LeuLysVal-----GlyLysTyrGluLysArgIleAspIle 236
Db 676 GGACTCATGATCTTACCAATTAACTTCCCTGGAACCACTCCATGATCTCCAGACT 735
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
Db 736 AAGAGAAATATGCTGAGCAAGTGAAGATATGAAGGCAAA-----ATTAGG 786
Qy 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeu 276
Db 787 AAAACAAGAACCAAGAGAGAGATGATGTTATTCGAAAGAGATT---GTGAGATGCTGG 843
Qy 277 LeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile***Gly 296
Db 844 CTTAAGACTCAAGTGAACAT-----TTAATCTCAAAATTGATGCTGCTAAC 888
Qy 297 LeuValValAsp***PheSerAlaGly***AspSerThrIle*****ThrGluTyrAla 316
Db 889 AATATGATCAACATGATGATCCTGCGCAGATTCGTCTCTGCTCATTAACCTTGCC 948
Qy 317 LeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSer 336
Db 949 GTCAAAATTCCTCTCTGATTTCTCTGCTGCGCCCTCAATCTCTAAGAAAACATGAAGCTG 1008
Qy 337 ValValGlyLysAsp***LeuValAspGluVal-----AspThrGlnAsnLeuPro 353
Db 1009 AAAAGTTTGAAGAAATGACAGAGAGCCACTATATGGAATGACTTACTGTTGCT 1068
Qy 354 TyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLys 373
Db 1069 TTAACACAAAAGGATTAACAGACACTGAGATGGAAAATGTTAATTTGAGATGATG 1128
Qy 374 ArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*** 393
Db 1129 AGAAGCGCATGAAGATGTTGAATTAAGATATGATATCAAAAAGATGCTGTTTC 1188
Qy 394 ***PheAsnValTpgGlnValGly***Asp***LysTyrTrpAspArgProSerGlu*** 413
Db 1189 TTGGCTATCTCATGATCAGTTACTCTTGAAGAGCTTATATGATGCTCCGTACAAATTT 1248
Qy 414 ArgProGluArgPheLeuGluTyr***AlaGluGlyGluAla*****LeuAspLeuArg 433
Db 1249 AATCCCTGAGAGATGCAAGAAAG-----GACATGAAC 1281
Qy 434 Gly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal*** 453
Db 1282 ACGAGTATGTTCACT-----CCTTTGAGAGTGTGTCAGAGATTTGCTCCGTCTCAT 1335

QY 454 LeuAlaThrSerGly**AlaThrLeuAlaSerLeuIleGlnCysPhe 470
1336 TTGGCTCGTCTTGAACCTTACGTTTCTTCACCATCTTGTCACTGCGCTTC 1386

RESULT 13
US-11-000-463-170
; Sequence 170, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weinman, Tom
; APPLICANT: Zhou, Jie
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ. ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 170
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(1814)
US-11-000-463-170

Alignment Scores:
Pred. No.: 8,4e-14 Length: 1882
Score: 183.00 Matches: 115
Percent Similarity: 33.58% Conservative: 68
Best Local Similarity: 21.10% Mismatches: 234
Query Match: 7.66% Indels: 128
DB: 7 Gaps: 22

US-09-857-581b-66 (1-521) x US-11-000-463-170 (1-1882)

QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu**ValLeuAlaLeuPhe**HisLeuArgPro 20
231 CTACTCTGCTGCTGGTGGTGGCTCTGGCTACTGCC-----CGATCTGGCT 261
QY 21 ThrPro**Ala**SerLySAlaLeuArgHisLeuProAsnProProSerPro**Pro 40
282 TGAACCTATGCTCTTAAACAACCTGCCGCCGCTCAAGTGTTCACACAGCCCCCAAA 341
QY 41 ArgLeuProPheIleGlyHis**HisLeuLeu-----LysAspLySLeuLeuHis 57
342 CGGAACGTGTTTGGGATCACCTGGGCTGATCTACTTACAGAGGAGGCTTTAAGAAC 401
QY 58 TyrAla**IleAspLeuSerLySHisGlyProLeuPheSer*****PheGlySer 77

DB 402 TGAACCAAGATGCGGCCACTTATCCAGAGGC-----TTTACATATGCTGGGTCC 455
78 ---MetProThrValValAlaSerThrProGluLeuPheLySLeuPheLeuGln***** 96
QY 456 ATCATCCCTTCATCGTTTATGCCACCTGACACCATCCGGCTATCCACATGCTCA 515
QY 97 GluAla-----ThrSerPhe**ThrArgPheGlnThrSerAla**Arg*** 112
516 GGTGCATTTGACACCAAGATATATCTCTTCATCAGGTT----- 554
QY 113 LeuThrTyrAsp*****ValAla*****Pro----- 123
555 -----CTGAAGCCCTGGCTGAGAGAGGATCTAGT 590
QY 124 ***GlyProTyrTrp**PheValArgLySLeuIleMetAsnAspLeu**AsnAlaThr 143
591 GGGGTGACAGATGGAGCCGCCACCGTGGATG-----CTGAGCCCGGCTTC 638
QY 144 ThrValAsn**LeuArgProLeuArgThrGlnGlnIleArgLyS**LeuArg**Met 163
639 CATTTCAATCTCGAAGTCTATATACG---ATCTTCAACAGAGTGCAACATCATG 695
QY 164 AlaGln-----**AlaGluAla**LysProLeuAsp**ThrGluGlu 178
696 CTGACAGATGGACGACCTGGCTCAGAGGCGACAGCTGTGTGACATGTTTGAAGAC 755
QY 179 LeuLeuLysTrp**AsnSerThr**SerMetMet**LeuGlyGluAlaGluGlu--- 197
756 ATC-----AGCTCATATACCTTGGACAGCTTACAGAAATGC 791
QY 198 IleArgAspIleAlaArgGluValLeuLysIle**GlyGluTyrSerLeuThrAspPhe 217
792 ATCTTCAAGCTTGAACGACCATTTGTACAGAGGCCAGAGATATATGCGAC----- 845
QY 218 Ile***ProLeuLys**LeuLysValGlyLysTyrGlnLysArgIleAspIleLeu 237
846 ATCTTGAAGCTCAGTCCCTT-----GTAGAGAAAGAGCAGCATATCTTC 893
QY 238 AsnLysPheAsp----- 241
894 CAGCAGATGACCTTTCTGTATTAACCTCTCCACGAGGCGGCTTCCACAGGCGCTGC 953
QY 242 -----ProValValGluArgValIleLysLysArgArg**IleValArgArg 257
954 CGCCTGTGATGATCTTACAGACGCTGATCCGGAGCGGAGTGCACCTCCACACT 1013
QY 258 Arg**AsnGlyGlu*****GluGlyGlu**SerGlyVal**LeuAsp-----Thr 275
1014 CAGGATATTGATGATTTTTCAAAGACCAAGCACTTCCACAGCTTGTGATTTCAATTGAT 1073
QY 276 LeuLeuGluPheAlaGluAspGluThr**GluIle----- 287
1074 GTGCTTCTGTGACAGAGATGAGATGGAGAGCATTGTACATGAGATATTAAGACA 1133
QY 288 ----- 289
1134 GAGCGTGAACCTTCATGTTTGGAGGGCTCAATATCTGGAGCGCTGTCCACCTCGGGTG 1193
QY 290 ThrLys*****Ile**GlyLeuValValAsp**PheSerAlaGly**AspSerThr 309
1194 CTGAACCAAGCTTACTGTGGCTGC-----TCCACAGCCATGACACACAGC 1238
QY 310 Ala*****ThrGluThrAlaLeuAlaGluLeuIleAsnAspPro**ValLeu***** 329
1239 GCCAGTGGCTCTCTGGGTCTGTACAACTTGGCAGGACCAACCAATATCCAGAGCGC 1298
QY 330 AlaArgGluGlu**TyrSerValValGlyLysAsp**LeuValAspGluVal----- 347
1299 TGCCGACAGAGAGGTGAAGAGCTTTC---AAGGACCGGATCTTAAAGATTTGAATG 1355
QY 348 ---AspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHis 366
1356 GACGACCTGGCCAGCTGCCCTTCTGACCATGTGCTGAAGAGAGCGTGAAGTTACAT 1415

[illegible]

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Db      1378 CTCGCCAAGTTAAATTTATTTATTTCTCCACATTAGTTTCCATTTCGATGGAA 1437
QY      474 ValLeuGlyProGlnGlyGlnIleLeuValGly***AspAlaIysValSerMetGluGlu 493
Db      1438 GTGAAGGAGGAGAG-----AAAGAAATACAGTACGATGCTCATTTCCAAATACCT 1485
QY      494 ArgAlaGlyLeuThrValPro---ArgAlaHisSerLeu 505
Db      1486 CAAAAGGCTCTCCCGCTACATTTCCGTGCACATTTCTT 1524

RESULT 15
US-10-995-561-81
; Sequence 81, Application US/10995561
; Publication NO. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-81

Alignment Scores:
Pred. No.:      3e-13      Length:      2361
Score:          180.00     Matches:      104
Percent Similarity: 34.38%   Conservative: 71
Best Local Similarity: 20.43%  Mismatches: 211
Query Match:      7.53%     Gaps:         123
DB:               6        Gaps:         20

US-09-857-581b-66 (1-521) x US-10-995-561-81 (1-2361)
QY      20 ProThrPro**Ala**SerIysAlaLeuArgHisLeuProAsnProProSerPro** 39
Db      147 CCATGTCCTGGCTGCGCTGACCTACGCTTCTATGACAACTGCCG---CCGCTTCGGTGT 203
QY      40 ProArgLeuProPheIle-----GlyHis***HisLeuLeu 52
Db      204 CCACAAACCCCCAGACGGAACCTGTTGGGGACACCAGGCGCATGATTACAGCTCAGA 263
QY      52 SAAPLyLeuLeuHisIleTyAla**IleAspLeuSerIysLeuHisGlyProLeuPhe 72
Db      264 AGAAGCTCTCTATACACAAAGCCTG-----GC 293
QY      72 r*****PheGlySerMet----- 78
Db      294 GTGCACCTTTGGGGATATGGGCTGCTGGTGGGGCCCTGGACAGGACATCCACAT 353
QY      79 -----ProThrValValAlaSerThrPr 86
Db      354 CTTTTCCTCCACGTCATCAGCTGTGCTCTTTGCTCCAGCTGCCATTTGACCAAGAA 413
QY      86 ogIleuPheIysLeuPheLeuGln*****GluAlaThrSerPhe**ThrArgPheG 106
Db      414 CAAGTTTCTTACAGCTTCTCGAGCCCTGGCTGGGGATGGGCTC----- 459
QY      106 nThrSerAla***Arg**LeuThrTyAsp*****ValAla*****Pro**GlyPr 126
Db      460 -----CTGCTGAGTGGCTGTGA 476
QY      126 oTyTrp***PheValArgIysLeuIleMetAsnAspLeu**AsnAlaThrThrValAs 146
Db      477 CAAGTGAGCCRCACCGCTGGAGT-----CTGACGCTTCCTTCCATTTCAA 524
QY      146 n***LeuArgPro-----LeuArgThrGlnGlnIleArg---Lys**LeuArg** 162

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Db      525 CATCTGAAGCCCTATATATGAGATTTTCAATGAGAGTGTGAACATCATGCACGCCAAGTG 584
QY      162 *MetAlaGln***AlaGluAla**LysProLeuAsp***ThrGlnIleLeuLeuLysTr 182
Db      585 GCAGCTCTGGCCCTCAGAGGDTATGTCCTGTTGGATATATGTTGACACATC----- 636
QY      182 p***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGlu----- 197
Db      637 -----AGCTCATGACCTTGACACGTCTACAGAAATGTGTCTTCAGCTT 680
QY      198 -----IleArgAspIleAlaAr 203
Db      681 TGACAGCATTGTGACAGAGAAACCCAGTGAATATATTTGCCGCACTTGTGAGCTCAGTGC 740
QY      203 gGluValLeuLysIle**GlyGluTySerLeu---ThrAspPheIle***ProLeu 222
Db      741 CTTGTATCAAAAAGACACCATGAGATCTCTCGCATATTTGACTTCTGTATTTATCTC-- 798
QY      222 s***LeuLysValGlyLeuTyTrGluLysArgIleAspAspIleLeuAsnLysPheAspPr 242
Db      799 -----ACCCCTGATGGCAGCGTTCCGACAGGGCCTGCCCTGTGTGCACAGACTTC----- 849
QY      242 oValValGluArgValIleLysLysArgArg**IleValArgArgArg***AsnGlyG 262
Db      850 ----ACAGATGCCGTCATCCAGAGCGCGCCGCACTCTCCCTAGCCAGAGTTTGATGA 905
QY      262 u*****GluGlyGlu***SerGlyVal**LeuAsp-----ThrLeuLeuGluPheAl 280
Db      906 CTTCTCTCAAGCCCAAGCCCAATTCACAGACTTTGACCTTCATTGATGTACTCTGCTGAG 965
QY      280 agIleAspGluThr**GluIleLysIleThrLys*****Ile**GlyLeuValValAs 300
Db      966 CAAGCATGAAGACGGGAAG---AAGTTATCTATATGACATATAGACGAAAGCTGACAC 1022
QY      300 p***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGlu 320
Db      1023 CTTTATGTTTGAAGGCGCATGACACACGCGCAGTGTCTCTCCGTGGTCTGTACCACT 1082
QY      320 uIleAsnAsnPro**ValLeu*****AlaArgGluGlu**TySerValValGlyLys 340
Db      1083 TGCAAAAGCACCCCAAGTATACAGAGCGCTGCGCGAGAGGTGCAGAAACTTCTG---Aa 1139
QY      340 SAAP***LeuValAspGluVal-----AspThrGlnAsnLeuProTyrlIleArgAl 357
Db      1140 GGAACGTGAGCCCTAAAGAGATTGAATGGAGACACCTGGCCATTGCCCTCTGTACACAT 1199
QY      357 aIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLysCys** 377
Db      1200 GTGCATGAAGAAGAGCTGGCGCTGCATCCCCAGTCCCGGTCACTCCCGCATGTCAAC 1259
QY      377 *GluGluCys**Ile---AsnGly***Val**ProGluGlyValLeu*****PheAs 396
Db      1260 CCAGACATTGTGCTCCAGACGCGCGGTGATCCCAAGGACATTATCTGCTCATACAG 1319
QY      396 nValTrpGlnValGly***Asp***LysTyTrpAspArgProSerGluu**ArgProG 416
Db      1320 TGTTTTCGAACCAACCATCACAAACCACTGTGTGTGCGGACCCCTGAGAGTCTACGACCCCTT 1379
QY      416 uArgPhe---LeuGluThr**AlaGluGlyGluAla*****LeuAspLeuArgGly** 435
Db      1380 TGCCTTTGACCCAGAGAAATCATCAAGAGAGTCACT----- 1416
QY      435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysPProGlyVal**LeuAl 455
Db      1417 ----CTGGCTTTTATTTCTTCTCGGCAAGGCGCCAGAGAACTGCATCGGGACAGCTTGC 1472
QY      455 aThrSerGly**AlaThrLeuLeu 463
Db      1473 GATGCGGAGATGAAGTGTCTCTG 1497

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Fri Dec 23 08:58:15 2005

us-09-857-581b-66.rnpbn

Page 17

Job time : 317 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 21:08:13 ; Search time 45 Seconds
(without alignments)
957.201 Million cell updates/sec

Title: US-09-857-581b-66

Perfect score: 2389
Sequence: 1 MLELALGLVLAFLXHLRP.....ASHLVCPILARIQVASKLS 521

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/iaa/5.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/H.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCBUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2250	94.2	521	2	US-08-948-564-14
2	944.5	39.5	512	2	US-09-672-785-4
3	940.5	39.4	506	2	US-09-672-785-2
4	921.5	38.6	506	2	US-09-672-785-8
5	651	27.2	513	2	US-09-351-229-4
6	637.5	26.7	508	2	US-09-142-108C-17
7	629	26.3	495	2	US-09-689-783A-2
8	626	26.2	512	2	US-09-142-108C-6
9	623	26.1	513	2	US-09-142-108C-15
10	618.5	25.9	496	2	US-09-292-768-2
11	618.5	25.9	496	2	US-09-292-768-66
12	615	25.8	496	2	US-08-881-784-1
13	615	25.8	500	2	US-09-292-768-4
14	615	25.8	500	2	US-09-292-768-68
15	615	25.8	512	2	US-09-142-108C-2
16	615	25.8	500	2	US-09-292-768-70
17	613.5	25.7	496	2	US-09-292-768-64
18	613.5	25.7	500	2	US-08-881-784-9
19	608	25.4	502	2	US-09-499-302A-2
20	606.5	25.4	496	2	US-09-172-335-6
21	602.5	25.2	471	2	US-09-126-420A-20
22	599.5	25.1	498	2	US-09-292-768-6
23	592	24.8	508	2	US-09-142-108C-19
24	590.5	24.7	500	2	US-09-142-108C-4
25	590	24.7	517	2	US-09-142-108C-21
26	583	24.4	516	2	US-08-948-564-12
27	574	24.0	496	1	US-08-313-075A-50

ALIGNMENTS

28	574	24.0	496	2	US-09-142-108C-41	Sequence 41, Appl
29	572	23.9	502	2	US-09-499-302A-4	Sequence 4, Appl
30	570.5	23.9	510	2	US-08-606-505B-66	Sequence 66, Appl
31	570.5	23.9	510	2	US-09-616-990-66	Sequence 66, Appl
32	567	23.7	476	2	US-09-142-108C-23	Sequence 23, Appl
33	566.5	23.7	476	1	US-08-313-075A-30	Sequence 30, Appl
34	564	23.6	523	2	US-08-606-505B-67	Sequence 67, Appl
35	564	23.6	523	2	US-09-616-990-67	Sequence 67, Appl
36	563.5	23.6	506	1	US-08-313-075A-38	Sequence 38, Appl
37	563.5	23.6	506	2	US-08-606-505B-65	Sequence 65, Appl
38	563.5	23.6	506	2	US-09-616-990-65	Sequence 65, Appl
39	562.5	23.5	513	2	US-09-142-108C-42	Sequence 42, Appl
40	561.5	23.5	514	2	US-09-947-027-4	Sequence 4, Appl
41	559.5	23.4	529	2	US-09-615-192A-405	Sequence 405, App
42	556.5	23.3	490	2	US-09-126-420A-16	Sequence 16, Appl
43	556.5	23.3	520	1	US-09-091-432-2	Sequence 2, Appl
44	556.5	23.3	520	2	US-09-387-663-2	Sequence 2, Appl
45	556.5	23.3	520	2	US-09-214-139B-4	Sequence 4, Appl

RESULT 1
US-08-948-564-14

; Sequence 14, Application US/08948564

; Patent No. 6121512

; GENERAL INFORMATION:

; APPLICANT: Siminszky, Balazs

; APPLICANT: Dewey, Ralph E.

; APPLICANT: Corbin, Frederick T.

; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and

; NUMBER OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants

; CORRESPONDENCE ADDRESSES:

; ADDRESS: Virginia C. Bennett

; STREET: PO Box 37428

; CITY: Raleigh

; STATE: No. 6121512th Carolina

; COUNTRY: USA

; ZIP: 27627

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/948,564

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Bennett, Virginia C.

; REGISTRATION NUMBER: 37,092

; REFERENCE/DOCKET NUMBER: 5051-409

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-854-1401

; TELEFAX: 919-854-1401

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 521 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-948-564-14

Query Match 94.2%; Score 2250; DB 2; Length 521;

Best Local Similarity 86.6%; Pred. No. 2.3e-273;

Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1 MLELALGLVLAFLXHLRPTXAXSKALRHLPPPSXPRLPTIGHXHLKDKILHYAX 60
Db 1 MLELALGLVLAFLXHLRPTXAXSKALRHLPPPSXPRLPTIGHLHLKDKILHYAL 60

Qy	61	IDLSSKHGFLSEFXHGSMTVAASAPELFLFLQXXEATSFXFRFOTSAKRLTYDXVA	120
Dd	61	IDLSSKHGFLSELYGSMPTVAASTELKFLFLQTHEATSFNTRFOTSAIRLLTYSVA	120
Qy	121	XXPKGPMYFVAKLIMNDLXNAITVNXLRPLRTOQIRKRLKMAQXAAXKPLDXTTELL	180
Dd	121	MVPFPGPMYFVAKLIMNDLXNAITVNXLRPLRTOQIRKFLRVMAQGEAKPLDLTEELL	180
Qy	181	KMXNSTXSMXKLGEAEITDIAREVUKITIGEYSLTPIYXKLKLYGKYEKRIDDLINKE	240
Dd	181	KWTNSTISMMKLGEAEIRDIAEVUKITIGEYSLTPIYWLKRLKGYEKYKRIDDLINKE	240
Qy	241	DPVEVERVIKKRRXIVARRRXNGEXXEGEXGVXLDTLLEFADEDETXEIKTRKXIXGLVVD	300
Dd	241	DPVEVERVIKKREIYARRKNGEYVEBESVSVPFLDTLLEFADEDETMELIKIKDHEGLVVD	300
Qy	301	XFSAGXGSTAXXTTEWALIELINNXYLLKXAREEXYSYVGKDLVDEVYTONLPYIRAIYK	360
Dd	301	FFSAGTGSTAVATTEWALIELINNPKYLEKAREBEVYSVVGKDRLVDEVYTONLPYIRAIYK	360
Qy	361	EFRRNHPLPYVYRKCKXECXIXGXYPBEGALTXFFNVMOVGXGXKYWDRESEKREPEAFLE	420
Dd	361	ETFRNHPLPYVYRKCKTEBCEIXGYIYPBEGALLLFNVMOVGGRPKYWDRESEFRPEPEFLE	420
Qy	421	TYABEGAXXLDLRGXHFOLLPFSSGGRXMCBGVXLATISGAXTLTLASLLIQCFDLYLGBGQG	480
Dd	421	TOABEGAGPLDRGQHFOLLPFSSGGRMCGVNLATISGMATLTLLASTIQCFDLYLGBGQG	480
Qy	481	ILKGDADAKYSMEERAGLTVPRASISYCVPLARIAGVASKLIS 521	
Dd	481	ILKGDADAKYSMEERAGLTVPRASISYCVPLARIAGVASKLIS 521	

```

RESULT 2
US-09-672-785-4
; Sequence 4, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Torenia hybrida
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
US-09-672-785-4
; OTHER INFORMATION: directly convert Flavonone to Flavone

```

[illegible]

```

QY 93 LOXXATEFPIRFOQSARXILTYDXXVXXXPKGYWXXFVRKLIIMDLNATVYNXLRPLR 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 87 LKTNB-LAFSSRKSHSTALDITVYDSSPAFSPYGPYWKYIKCLCTYELLGARNIGHFQPIR 145
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 153 TQOIRKXILRMAOXAABKPLDXTTELLKKNKSTYSMNL-----GEAEIPIQIARE 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 146 NLEVASFLQILMHKSPKQESVAVTDELVALNTSTNVLSHMLSLRCSSEBDQAEARVPIRE 205
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 205 VLKIGEYSLTFDPIKPLKXKVKYEKRIDDLINKFDPVVEHVIKKRRXIIVRRRXNGEXX 264
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 VTQIRGEVDVDDIIFWCKKFKDLOQIKKSESDIQRRYDALLEKTIISRER--SRQRORDKH 263
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 265 BG---EXSGVXLDTLLEPADETFXIKITKXXIXGLVNDXFSQXSDSTAXXTFWMALBL 321
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 264 GGGNNEEAKDFLMDLLDVWESGDTFVKKFRRHKLKILDFFTAGTDTTIAATEWALAEI 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 322 NNPKYLLXXAREXSVSGKDXLVNDVDPONLRYIRAIIVETPRMHPLPVPVKKCEBX 381
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 NNPNVLKKAQOEISRIIGTKRIVQSDADPLYLQIIMETRLHPPIPLWSKKSISDCT 383
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 382 INGVXYPGALATXFPVWVQGXDKXKWDRPSEKXPERFLETXAEGAXXXLDLRGXHFQLLP 441
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 384 VNGVYIKQAKSLLFVNIWMSIGRPNPWSMEPRPERFLEKGR-----SIDVQGHFELP 439
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 442 FSGGKXMCBQVYXLAISGAXTLIASLIQCDPDLVYLGQOQILKGDAXKVSNEEBAAGLTVP 501
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 440 FGTGRRGCGEMLALQEVVSIIGTWQCPD-----WKLADSGNNVMDTERTSGLTAPR 492
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 502 AHSIWCVPFLARIGVAS 517
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 493 APDVLVCRLYPRVDPAT 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

US-09-672-785-2      RESULT 3
; Sequence 2, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kazumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672.785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JPO0/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JPO0/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-2

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Query Match	39.4%	Score	940.5	DB 2	Length	506
Best Local Similarity	39.8%	Pred.	6.7e-109			
Matches	196	Conservative	86	Mismatches	185	Indels
					25	Gaps
					9	

QY	30	RLLNPSPSXRPRLPRITGHHLLKDLTAYAKIDLSKKHGLPSXSSXGSMPTVVASTPELF	89
DB	24	RKRTRPPGGL-ALPLIGHMLGPKR-LHHTTRHFSQRKQGLPLQLQLYLSSPCVASTPELA	81

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QY 90 KLFLOKXEATSPKTEPQISAXBKLTYYDXVAXXPKGPYMXFVRLKIMMDLXNAITTVXKLR 149
Db 82 REFLLKTHE-LDBSSRGHSTAIIDITVYDSSFAPAPYGPYWKFTIKCLCTYELLGAINSHFQ 140
QY 150 PLRTQOIRKCLKXMAQXAEAKRPDXTEELLKWNSTYSMMXL-----GEAEIRDI 201
Db 141 PIRALEVNSFLRLIYEKTEQKOSVNVTEBELVLTLSNVISNNMGLGRCSGTEGEAEVARTV 200
QY 202 AREVYLKIXGEYSLTDPYIXPLKYLKXGKYEKRIIDLIINKEPDPVBEVHKREKXIRRRXNG 26
Db 201 IREVTOIIFGEFVDSEIWFCEKMDLOGIRKRESEDIRRRYDALLEKXISDRERL-RLRGCG 25
QY 262 EXXEGEXSGVYLDOTLLEFADEETXEIKIRKXXIXGLVNDXSPAGXDSTAXXTWEMAEI 321
Db 260 GGGGGGVKQD-FIDMLIDVDNESEKSEBVEFRELHKALJIDPFYAGDTTIAITTEMAIELI 318
QY 322 NNFXVYLXXAREEYXSVGKDXLVDEVDTONLPIYITAIYKETFRRMHPPLPYVKRKCBECK 38
Db 319 SNBNVILKXQOEEMDKVIGSORLLQESBDANLPELYNAAIIKEFTFRLLPIPLMLTRISISDV 376
QY 382 INGVXVPBGALXXXFNWOWGXDKKYDRPSEKRPSEFLTXAEGEAXXLDLRGXHFOLDP 441
Db 379 VNGYTIIPAKTLLFVNLMMSGMRNNTYENEMERPREPELEKG----TGSIDVKGQHFELLP 433
QY 442 FGSGRXMXCPGVXLATSGXATLTLASLIIOCFDLOVLGPQOILKGXDAKYSMEBRAGLYPR 501
Db 435 FGTRGRRCPCPMLGMOBELFSIIGAMVQCFQDMKL--PDGV-----KSYVDTERPEGLTAPR 486
QY 502 AHSLYVCVPLARI 513
Db 487 ANDILVQOLVPR 498

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RESULT 4
US-09-672-785-8
Sequence 8, Application US/09672785
Patent No. 6596927
GENERAL INFORMATION:
APPLICANT: Mizutani, Masaaki
APPLICANT: Kaesumi, Takashi
APPLICANT: Akashi, Tomoyoshi
TITLE OR INVENTION: Genes Coding for Flavone Synthases
FILE REFERENCE: 001560-383
CURRENT APPLICATION NUMBER: US/09/672,785
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP00/04379
PRIOR FILING DATE: 2000-01-30
PRIOR APPLICATION NUMBER: PCT/JP00/00490
PRIOR FILING DATE: 1999-01-28
PRIOR APPLICATION NUMBER: JP 11-205229
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: JP 11-22427
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 506
TYPE: PRT
ORGANISM: Perilla frutescens
FEATURE: Amino acid sequence of a protein having an activity to
OTHER INFORMATION: directly convert Flavonone to Flavone
US-09-672-785-8

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	Query Match	38.6%	Score 921.5	DB 2	length 506
	Best Local Similarity	38.9%	Pred. No. 1	6e-106	
	Matches 190	Conservative 91	Mismatches 183	Indels 25	Gaps 8
Qy	33	PNPSPDXPLPTIGXHLKDKLHYAKIDLSKKGGPFLSSXFGSNPYPVASTBPLFLKLF	92		
Db	27	PYPGPGPP-LPTIGHLHLGGPR-LHOTPFHDSQRFQGGPMLQQLGSLSTRCVIAASPELAEAC	84		

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OY 93 LQXKXETSPXTEFOQSAXRBLTVYXXVXXEXGPMXKFEVRLLIMNDLXNTVYXLRPR 152
OY 85 LKTHELV-FSSKHSHTAIDVYTBDSFSPFSGYGMFKFIKTLCTYELLGARNLHNPFR 143
OY 153 TQOIRKCLRXMAQXBAKKPDLXTEELLKMXNSTXSMXL-----GEAEIRDIARE 204
Db 144 TLEVKSFQILMRKSGSGSFVTEVELKLTNSNYISHMULSIRCSETESEAEARVIRE 203
OY 205 VLIKXEBYSLTDFIKPLKLLKVGKXKERIDILLKPRPVVERVKKGRXLYVRBXNEXX 264
Db 204 VTQIFEEFVSIDILWLCXNPFQGRKXSEBIOQRVYDLLEKITTDEK--QRRTHGGG 261
OY 265 EGEXSVAXLDTLLEFAEBETXEIKITKXXIXGLVWDXFSAGXSDTAXXTMALAELINP 324
Db 262 GGGEADPFLMFLDIMESGAEVKFTREHLKALILDFPTAGTPTTALVCEMALEVINP 321
OY 325 XVLXXAREEXYSVYGKDLVDEVDVQNPPIYRALVKEFFRNHRLPVVXKCKBECKING 384
Db 322 NVLKKAQEBEIANIVGDFRILLOESDAPNLPYLOALIKETFRHPRLPMLARKSSIDCVIDG 381
OY 385 XVXPEGALKXFPNWQYGDXXKWDPRSEKXPERPLETAYABGEAXXLDLRGNHOLLPGS 444
Db 382 YMLPANTLLEVNLMMSGNRPKIMDVPFLPAFORPERLEK-----EKAIDVKGQHFELPFGT 437
OY 445 GRXKCPGVXLIATSGAATLLASLLOCFDLOVLGPOQILKGDATVYSNEERAGLTVPRAS 504
Db 438 GRGCGCGMMLAIOEVLVIIGTWIOCFPMWL--PDG-----SGHVMAERBGLTAPRETD 488
OY 505 LVVCVPLARI 513
Db 490 LFCXVPRV 498

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RESULT 5
US-09-351-229-4
; Sequence 4, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; CURRENT FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Zea mays
US-09-351-229-4

```

[illegible]


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QY      25  RXIVRRRXNGEXXEGXSGVXLDTLFEADETXEIKTKKXIXGLVVDXSASQJSTAX 31.1
Db      264  RL-----REGGNFAKD-----MDVLLQLADDTSLSEVLQSRDNVKAITDDLLIAGTDSNAN 31.5
QY      312  XTEWALAEILINNDYLVXXARBEEXYSVVGKDXLVDEVDTONLPYIRAIKETEFGNHPPLPV 371.1
Db      316  TLEWASELLKNPKRIITAKAMEEILNHVIRPDRIJVTESDIPRLPYIEAVLKEFMRVHPAPM 375.5
QY      372  V-RRKCKEBCIXNGXYXPEGALXXPFVMOVGDXKYWRMPSEKRPREFLEFXAGGAXXL 430.0
Db      376  LAHVVARIEDTSVDGYDLAGTVLFINVAALIGDPCGLMDAPPEEFRRERKVES-----KI 428.8
QY      431  DLRGXHFOLLPFSSGRXMCPEVXLATSGXATLLASLIQCFDLQVIGPQGQILKXGDAKVS 490.0
Db      429  DVGCHDFOLLPFSSGRMCPGIMATLKVMALSLANILHGFEMRL--PGVTAAE----ELS 482.0
QY      491  MEERAGLTVPRAHSILYCVPLAARI 513
Db      483  MDEAFKLAIVRKFPLMVVAEPRL 505

```

RESULT 6
 US-09-142-108C-17
 ; Sequence 17, Application US/09142108C
 ; Patent No. 6774285
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruggliera, Filippa
 ; APPLICANT: Holton, Timothy A.
 ; APPLICANT: Michael, Michael Z.
 ; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; FILE REFERENCE: 11658
 ; CURRENT APPLICATION NUMBER: US/09/142,108C
 ; CURRENT FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: PN8386
 ; PRIOR FILING DATE: 1996-03-01
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 508
 ; TYPE: PRF
 ; ORGANISM: Chrysanthemum
 ; US-09-142-108C-17

Query Match	26.7%;	Score 637.5;	DB 2;	Length 508;
Best Local Similarity	30.7%;	Pred. NO. 7.7e-71;		
Matches 162;	Conservative 101;	Mismatches 208;	Indels 57;	Gaps 14;

Oy	5	IAGLXVLAIFXHLRPTPXKXSKALNHLNPPSPXP-RLPFGIHXHLDKILYHXI	61
Db	11	LIIG-SLYLV/LNL-----SSRKXARLPPGPTMVIYONLPHLG-----PIPHNALA	56
Oy	62	DLKKHGPRFSXXFGSNPTVYASTPELFLKFLDLOXEAHSFXTRPQTSAXKXILYD-XVVA	120
Db	57	ALAKKQYPLMHLKLCGDVVVAASASVAOFLKHMDA-NFASRPNPSGAKVVAANYODLV	115
Oy	121	XXRXPWXXFVRKLIIMVDLKNATTVXKLRPLTQOIRKCLRMAOXAEKXKRLDXTBEIL	180
Db	116	FAPYGPFRMLLRKICSHLPSAKALDPRHVHQEEVAVLTVLLSAGNS--PVQIGQGLN	173
Oy	181	KKXNISTXSMKKLG-----EAEIRDLAEVLKIXGEISLDFIXPLKYLKVGKYE	233
Db	174	VCATNALARWLGRVFGDGDIDRSANEPKDMVVELVNLAGEPNLDDFIPLVLDPLQGIT	233
Oy	231	KRIDIDINFRPVVERVIKKRKRIYBRKXNGEXXEGXSGVILDTLFEAEDETVE-IKI	285
Db	234	KMKKKLHVRRDSFLSKIVEHKT-----APGGLGHTDLSLTLISLKDDADIEGKXL	286
Oy	290	TKXXIXGLVVDXBSAGKDSIAXXTBMALAEILINNPRVLLXXABEXKSYVGKDLVDEYDT	344
Db	285	TDEIKALLNLNFAAGGTSSSTVEWAIIEILLNHPDILQAAEEEDIDAVVGQDRVLTEDL	344

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Oy 350 QNLRYRALVKEPRFNNRPLPV-VRKCKXEECXNGXVREGALXXFNWQVGDXXCYMD 408
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 408
Db 345 SOLTYQALVKEFRFHHBPSTLSRISSECBEGDYITKGSITLLNVMAIARDPQMA 404
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 404

Oy 409 RPEXRPBERFLETXAEGEAXXLDRGKHFOLLPGSGRXYMCPGYALTSQATLTLASIQ 468
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 468
Db 405 DPLEFRPSRPL---PGEGKPGADVAGNDFVIYFPGAGRRITAGNSLSGLRWQQLITLVQ 461
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 461

Oy 469 CPDLOY---LGPQGOLIKGDXAKVAMEERAGLTVPRAHSLVCVLIARI 513
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::| 513
Db 462 TFWMEIANGLEBP-----MLNMEAYGLTILORAAPLMVHKKRPL 500
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RESULT 7
US-09-689-783A-2
; Sequence 2, Application US/09689783A
; Patent No. 6605469
; GENERAL INFORMATION:
; APPLICANT: KANG, JEONG-GU
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A CYTOCHROME P450 HYDROXYLASE IN
; TITLE OF INVENTION: BRASSINOSTEROID BIOSYNTHESIS IN PLANTS
; FILE REFERENCE: 107572
; CURRENT APPLICATION NUMBER: US/09/689,783A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-689-783A-2

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Query Match	26.3%	Score 639; DB 2;	Length 495;
Best Local Similarity	31.8%	Pred. No. 8.7e-70;	
Matches 156; Conservative	85;	Mismatches 192;	Indels 58; Gaps 13;

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QY 35 PPSKPRPLPGIGHXHLKDKLHVAHIDSKKHGPFSSXFGSGMPYVASTBELFKJLELO 94
Db 36 PPGPRP-WPIJENFWLI--GTLPHQSLHGLTOKGPIIMHLMFGSKRVVVGSTVEAKAFK 93
QY 95 XKEATSPYTRFQOTSAXRXLTYD-XXVAXXPXGPMYFVRKLIMNDLXNATTVXKLRLPT 153
Db 94 THDAI-LNGRPRFSAKTYTTNYSDITWGOYGPYMRQARMCLLELFSARLESYEYIRK 152
QY 154 QOIRKXLRMAQXAEAXKPLDXTEELLKMXNSTXSMKLG-----EAEIRDI 201
Db 153 QELHVFLEHLFDSRN--KTILLKDHLSLSLNIWISHWLVGRKYLEKVENSIISPDEPKNM 210
QY 202 ABEVLKIXGEYSLDTPIFXKLKLVKTEKRIIDLINLKRPPVVERVYIKKRRXIYRRXNG 261
Db 211 IDLEFLNLGILNIGCFIPWIFHFLDFOGYVKRMVLSEKPFGEFMEHVLSEH--IERRK-- 265
QY 262 EXXEBEXSGV-----XLDPTLEFADEDTXEIKIRKXXIXGLVVDPFASGXIDSTAXTE 314
Db 266 -----GVKDYYAKDMVDVLLQGLAEDPDLEKLEHGVKATQODLIAGSTESSAYVE 317
QY 315 WALAEILNPNXYVLXXAREEXYSVGKDXLVDEVDTONLPYIRAIYKTEFPMHPRP--VVK 373
Db 318 WAISELIRKPELFKXATEELDRVIGERWVEEKDINLPRVYAIKACTMHLNPAVPMIVP 377
QY 374 RKCXEECKINGXVDEGALXXFNWQOVGXDKXKYWDRPSEKRPREFLETXAEGEAXXIDLK 433
Db 378 REARDEDNINGVDIRKGSLLIVNTWTIARDSNWDMNPEMPPRFL-----GKIDIVK 430
QY 434 GCHFOQLPFGSGRMCPGVXKATSGAXITLALSLIOCFDLQVLGRQOILKGDAX---VS 490
Db 431 GHDYELLPGAGRRMCPGYPLGIVLQSSILANLHGFNMWL-----SDVKKEDLN 481
QY 491 MEERAGLTWPR 501
Db 482 MEERFGLSTPK 492

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1      INFORMATION FOR SEQ ID NO: 1:
2      SEQUENCE CHARACTERISTICS:
3          LENGTH: 496 amino acids
4          TYPE: amino acid
5          STRANDEDNESS:
6          TOPOLOGY: linear
7      MOLECULE TYPE: protein
8      ORIGINAL SOURCE:
9          ORGANISM: Mentha spicata
10         IMMEDIATE SOURCE:
11         CLONE: SM12.2
12     FEATURE:
13         NAME/KEY: Cleavage-site
14         LOCATION: 7..27
15     OTHER INFORMATION: /note= "V-8.2 proteolytic fragment"
16     FEATURE:
17         NAME/KEY: Active-site
18         LOCATION: 7..48
19     OTHER INFORMATION: /note= "Membrane insertion"
20     OTHER INFORMATION: sequence"
21     FEATURE:
22         NAME/KEY: Active-site
23         LOCATION: 44..48
24     OTHER INFORMATION: /note= "Halt-transfer signal"
25     FEATURE:
26         NAME/KEY: Cleavage-site
27         LOCATION: 182..206
28     OTHER INFORMATION: /note= "V-8.1 proteolytic fragment"
29     FEATURE:
30         NAME/KEY: Cleavage-site
31         LOCATION: 380..404
32     OTHER INFORMATION: /note= "V-8.3 proteolytic fragment"
33     FEATURE:
34         NAME/KEY: Binding-site
35         LOCATION: 429..454
36     OTHER INFORMATION: /note= "Heme binding region"
37     US-08-881-784-1

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OY 496 GLTIVRAHSIWCVP 509
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 Db 477 GLSGPKKKNVCLVP 490

RESULT 13
 US-09-292-768-4
 ; Sequence 4, Application US/09292768
 ; Patent No. 6194185
 ; GENERAL INFORMATION:
 ; APPLICANT: Croteau, Rodney B
 ; APPLICANT: Lupien, Shari L
 ; APPLICANT: Karp, Frank
 ; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
 ; TITLE OF INVENTION: LIMONENE HYDROXYLASES
 ; FILE REFERENCE: waur13463
 ; CURRENT APPLICATION NUMBER: US/09/292,768
 ; CURRENT FILING DATE: 1999-04-14
 ; EARLIER APPLICATION NUMBER: 08/881,784
 ; EARLIER FILING DATE: 1997-06-24
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Mentha piperita
 ; US-09-292-768-4

Qy	436	HFOILLPGSGRMCGVXILATSGAKTTLASLIJCEFDVLGFGOQIIKGDADAKYSMEERA	495
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	:	: : : : :	
	:	: : : : :	
Db	423	DEEFLPFGGRICIGLHFGULANVEIPLAOLLYHDWYL--POQM---TDADLLMTETP	476
	:	: : : : :	
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RESULT 14
US-09-292-768-68
; Sequence 68, Application US/09292766

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/ Patent No. 6194185
/ GENERAL INFORMATION:
/ APPLICANT: Croteau, Rodney B
/ APPLICANT: Lupien, Shari L
/ APPLICANT: Karp, Frank
/ TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
/ TITLE OF INVENTION: LIMONENE HYDROXYLASES
/ FILE REFERENCE: wbu13463
/ CURRENT APPLICATION NUMBER: US/09/292,768
/ CURRENT FILING DATE: 1999-04-14
/ EARLIER APPLICATION NUMBER: 08/881,784
/ EARLIER FILING DATE: 1997-06-24
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 68
/ LENGTH: 500
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
US-09-292-768-68
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Query Match      25.8%; Score 616.5; DB 2; Length 500;
Best Local Similarity 29.6%; Pred. No. 3.3e-68;
Matches 145; Conservative 91; Mismatches 207; Indels 47; Gaps 11;
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DB 36 PPGP-PKLPILGHLHLWGKLPQHALLASVAKQGPVAVHQLGEVFSVLSREATKAMK 94
QY 95 XHEATSPFRTQTSAXRKLTYD-XXVAXXPXGPYXKLVKLMNDLXNATTYNXLRPLRT 153
DB 95 LVD-PACADRFESIGTKIMWYDNDITFSPYSVHWKQMKICVSELSARNVRSFGFIKQ 153
QY 154 QOIRKXLRMAOXAAKXPLDYTEELLKXNSTXSMMXLG---EAEIRDIAREVLKIX 209
DB 154 DEVSLHLGHRSSAAAGEAVDLTERIATITCSIIICRAAGSVIRHHELVKXALMSA 213
QY 210 GEYSITDFIXPLKXL-----KVGKYEKRIDILINKPDEVVERVIKRRXIVRRKNG 261
DB 214 SGFEILDMPSSSKLNLICWNKSKLBRMRBYDALIEAI--VEBHKLKK----- 260
QY 262 EXXBEEXGV-XLDTLLFEADETYEIKTKXXIXGLVVDXFSAGXDSITAXXTWMALE 320
DB 261 ---SEFGEEDIIIDVLFEMQKDSQIKVPIITTAIKAFIDTFSAGETISSTTLWMAEL 317
QY 321 INNPVYLXXAREEXYSVGVKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPVVKRKCXEEC 380
DB 318 MRNPEVMAKQAQAEVAAALAGKTDMDVDVQELKTKMSVYKETMRNHPPLIPRSCREEC 377
QY 381 XINGXVXPEGALXXFNVMQVGVXDXKXWDRPSXRPREFLETYAEGEAXXLDLGGXFPOLL 440
DB 378 EVNGYTIIPKARIMINVMGMRNPLYWEKETFWPERF-----DQVSRDFMGDFEPI 430
QY 441 PRGSGRXMCPGVXALTSXATILASLIQCFDIQVLGPOQIILKGD-AVNSHEEBAGLTV 499
DB 431 PFGAGRRIICPGLNFGLANVEPLAQLLYHFD-----WKLAEGMNPDSMDSEAGLGTG 483
QY 500 PRAHSLVCP 509
DB 484 IRKNMLLVF 493
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RESULT 15
US-09-142-108C-2
/ Sequence 2, Application US/09142108C
/ Patent No. 6774285
/ GENERAL INFORMATION:
/ APPLICANT: Bruguiera, Filippa
/ APPLICANT: Holton, Timothy A.
/ APPLICANT: Michael, Michael Z.
/ TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
/ TITLE OF INVENTION: AND USES THEREFOR
/ FILE REFERENCE: 11658
/ CURRENT APPLICATION NUMBER: US/09/142,108C
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/ CURRENT FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: PN6386
/ PRIOR FILING DATE: 1996-03-01
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 512
/ TYPE: PRT
/ ORGANISM: Petunia x hybrida
US-09-142-108C-2
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Query Match      25.8%; Score 616.5; DB 2; Length 512;
Best Local Similarity 30.7%; Pred. No. 3.4e-68;
Matches 153; Conservative 96; Mismatches 209; Indels 41; Gaps 13;
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QY 92 FLQXXEATSPFRTQTSAXRKLTYD-XXVAXXPXGPYXKLVKLMNDLXNATTYNXLRP 150
DB 89 FLKTHDA-NFESSRPPNSGAEHMAVNYQDLPVAPYGRWRMLRKICSVHLFSTKALDDPRH 147
QY 151 LRTQOIRKXLRMAOXAAKXPLDYTEELLKXNSTXSMMXLG-----EAE 197
DB 148 VRODEVKLTITLALASAGQ--KPVKLGQLLVCTTNALARVMLGKRVFADSGGDVDPQAAE 205
QY 198 IRDIAREVLKIXGEYSITDFIXPLKXLKVGKYEKRIDILINKPDEVVERVIKRRXIVRR 257
DB 206 FKSXVYEMMVAVAGVFNIDFIFQLNWLIDIQVAAKMKLHARFADFLLDIEBHNG---- 261
QY 258 RXNGEXXEGEXGVXLDLLEFADETYEI--KITKXXIXGLVVDXFSAGXDSITAXXTW 315
DB 262 KIFGEMKD-----LSTLISLKDNDADNDGKLTDEIKALLNLFFVAGTDTSSSTVEW 315
QY 316 ALAEILNPPVYLXXAREEXYSVGVKDXLVDEVDTONLPYIRAIYKETFRRMHPPLPV-VKR 374
DB 316 AIAELIRNPKLIAQAOEIDIKVGRDRLVGBELDIAQLTYLBAIYKETFRRHPSFPLSPR 375
QY 375 KCXEXCXINGXVXPEGALXXFNVMQVGVXDXKXWDRPSXRPREFLETYAEGEAXXLDLGG 434
DB 376 IASBCEINGYIFPKGSTLLNVMNAIADPNAMADPLEFRERRL---PGGEKRVNDVRG 432
QY 435 XHFOLLPPSGRXMCPGVXALTSXATILASLIQCFDIQVLGPOQIILKGDADAKVSMER 494
DB 433 NDFEYIIPGAGRRIICAGNMLGIRMVQLMIAITLIHAFNMDLV--SGQL-----PEMLMEEA 486
QY 495 AGLIYVRAHSLVCPPLARI 513
DB 487 YGLTIQRADPLVHPRRL 505
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Job time : 47 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 22, 2005, 00:04:04 ; Search time 260 Seconds
(without alignments)
3561.960 Million cell updates/sec

Title: US-09-857-581b-66

Perfect score: 2389
Sequence: 1 MULTIALGXVLAEXHLP.....ASHLVCVPLARIGVSKLAS 521

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Fgapop 6.0 , Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2250	94.2	1824	3	US-08-948-564-13 Sequence 13, Appl
2	944.5	39.5	1730	3	US-09-672-785-3 Sequence 3, Appl
3	943.5	39.5	1724	3	US-09-672-785-1 Sequence 1, Appl
4	921.5	38.6	1770	3	US-09-672-785-7 Sequence 7, Appl
5	637.5	26.7	1660	3	US-09-142-108C-16 Sequence 16, Appl
6	629	26.3	1488	3	US-09-688-783A-1 Sequence 1, Appl
7	626	26.2	1711	3	US-09-142-108C-5 Sequence 5, Appl
8	625	26.2	1781	3	US-09-499-302A-1 Sequence 1, Appl
9	623	26.1	1748	3	US-09-142-108C-14 Sequence 14, Appl

10	618.5	25.9	1762	3	US-08-881-784-5 Sequence 5, Appl
11	618.5	25.9	1762	3	US-09-292-768-1 Sequence 1, Appl
12	618.5	25.9	1762	3	US-09-292-768-65 Sequence 65, Appl
13	618	25.9	1806	3	US-09-351-229-3 Sequence 3, Appl
14	616.5	25.8	1665	3	US-08-881-784-8 Sequence 8, Appl
15	616.5	25.8	1665	3	US-09-292-768-3 Sequence 3, Appl
16	616.5	25.8	1665	3	US-09-292-768-67 Sequence 67, Appl
17	616.5	25.8	1789	3	US-09-142-108C-1 Sequence 1, Appl
18	616.5	25.8	1665	3	US-09-292-768-69 Sequence 69, Appl
19	613.5	25.7	1762	3	US-09-292-768-63 Sequence 63, Appl
20	606.5	25.4	1762	3	US-09-172-339-5 Sequence 5, Appl
21	600.5	25.1	1515	3	US-09-292-768-5 Sequence 5, Appl
22	593	24.8	1815	3	US-09-142-108C-18 Sequence 18, Appl
23	590.5	24.7	1737	3	US-09-142-108C-3 Sequence 3, Appl
24	590	24.7	1824	3	US-09-142-108C-20 Sequence 20, Appl
25	583	24.4	1657	3	US-08-948-564-11 Sequence 11, Appl
26	578.5	24.2	1722	3	US-09-033-055A-1 Sequence 1, Appl
27	574	24.0	1757	2	US-08-313-075A-49 Sequence 49, Appl
28	574	24.0	1757	3	US-09-142-108C-26 Sequence 26, Appl
29	571.5	23.9	2174	3	US-08-606-505B-63 Sequence 63, Appl
30	571.5	23.9	2174	3	US-08-606-505B-63 Sequence 63, Appl
31	567	23.7	1667	3	US-09-616-990-63 Sequence 22, Appl
32	566.5	23.7	1665	2	US-08-313-075A-29 Sequence 29, Appl
33	565.5	23.7	1893	2	US-08-532-065B-1 Sequence 1, Appl
34	564.5	23.6	1927	3	US-08-606-505B-64 Sequence 64, Appl
35	564.5	23.6	1927	3	US-09-616-990-64 Sequence 64, Appl
36	563.5	23.6	1812	2	US-08-313-075A-37 Sequence 37, Appl
37	563.5	23.6	1824	3	US-08-606-505B-1 Sequence 1, Appl
38	563.5	23.6	1824	3	US-09-616-990-1 Sequence 1, Appl
39	561.5	23.5	1764	3	US-09-947-027-3 Sequence 3, Appl
40	559.5	23.4	2013	3	US-09-615-192A-404 Sequence 404, App
41	557.5	23.3	1634	3	US-09-126-420A-2 Sequence 2, Appl
42	556.5	23.3	1737	3	US-09-126-420A-1 Sequence 1, Appl
43	556.5	23.3	1838	2	US-09-091-432-1 Sequence 1, Appl
44	556.5	23.3	1838	3	US-09-387-663-1 Sequence 1, Appl
45	556.5	23.3	1838	3	US-09-214-139E-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-948-564-13
Sequence 13, Application US/08948564
Patent No. 6121512
GENERAL INFORMATION:
APPLICANT: Simmsky, Balazs
APPLICANT: Dewey, Ralph E.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
METHOD OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512ch Carolina
COUNTRY: USA
ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,564
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 5051-409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400

TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1824 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 54..1616
US-09-857-581b-66 (1-521) x US-08-948-564-13 (1-1824)
Alignment Scores:
Pred. No.: 1,32e-300 Length: 1824
Score: 2250.00 Matches: 451
Percent Similarity: 86.56% Conservative: 0
Best Local Similarity: 86.56% Mismatches: 70
Query Match: 94.18% Indels: 0
Gaps: 0
US-09-857-581b-66 (1-521) x US-08-948-564-13 (1-1824)
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Db ATGTTGCTTGAACCTTGCACCTGGTTTATGGTTTGGCTGTGTTTCGACCTTGGCGTCCC 113
QY 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
Db AACACCCATCGCAAAATCAAAAGACATTCGCCATCTCCCAAAACCACCAAGCCCAAGCCCT 173
QY 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisLysTyrAla*** 60
Db CGCTTCCCTTCAATAGACACCTTCATCTCTTAAAGACAACTTCTCCATCGACATC 233
QY 61 IleAspLeuSerLysLysHisGlyProLeuPheSer****PheGlySerMetProThr 80
Db ATGACCTCTCCAAAAAATGATGCTCTTATTCCTCTCACTTGGCTCCATGCCAAC 293
QY 81 ValValAlaSerThrProGluLeuPheLeuPheLeuGln****GluAlaThrSer 100
Db GTGTGTGCTCCACACACGAAATGTTCMACTCTCTCCCAACGCAAGGCAACTTCC 353
QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
Db TTCAACACAAAGGTTCCAAACCTCAGCCATTAAGACGCTCACTGATGACTCAGTGGCC 413
QY 121 ****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu*** 140
Db ATGTTTCCCTTGGACCTTACTGGAAGTTCGTAGAGAACTCATCAGAACGACCTTCCC 473
QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
Db AAGCCACACCACTGTAACAAGTTGAGGCTTTTGAGGACCCCAACAGACCCCAAGTTCCT 533
QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGlnGluLeu 180
Db AGGGTTATGGCCCAAGGCGAAGGCAAGAGCCCTTCACTTGAAGGCGAGAGCTTCTG 593
QY 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGlnIleArgAsp 200
Db AATATGACCAACAGCACATCTCATATGATGTCGGCAGAGGTGAGGATCAAGAGAC 653
QY 201 IleAlaArgGluValLeuLysIle***GlyGlnTyrSerLeuThrAspPheIle***Pro 220
Db ATGCTCGCAGAGGTTCTTAAGATCTTTGGCAATACAGCCTCACTGACTCATCTGGCCA 713
QY 221 LeuLys***LeuLysValGlyLysTyrGlnLysArgIleAspAspIleLeuAsnLysPhe 240
Db TTGAAGCATCTCAAGGTTGAGAAATATGAAAGAGATCAAGACATCTTGAACAGTTC 773
QY 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db |||||

Db 774 GACCTGTGCTTGAAGAGGTATCAAGAAAGCCCGTGAAGATGATGAGAGAGAAAGAAC 833
QY 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuGlnIlePheAla 280
Db GAGAGAGTTGTTGAGAGGTGAGGTCAAGCGGGGTTTCTTCTGACATCTTGTAATTCGCT 893
QY 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
Db GAGATGAGACCATGAGATCAAAATCAACCAAGACACATGAGAGGTCTTGTTCGAC 953
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGlnTrpAlaLeuAlaGluLeu 320
Db TTTTCTCGGACAGAAAGACTCCACAGCGGTGCAACAGATGGGCAATGGCAGAACTTC 1013
QY 321 IleAsnAsnPro***ValLeu*****AlaArgGlnGlu***TyrSerValValGlyLys 340
Db ATCAACAAATCCTAAGTGTGTGAAAAGGCTCGTGAAGAGCTCTACAGTGTGTGGAAAAG 1073
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db GACAGACTGTGAGCAGAACTTGACACTCAAACTTCTTACATTAGACCAATCGTGAAG 1133
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys**GluGlnCys 380
Db GAGACATTCGCGATGACCCGCCACTCCAGTGTCAAAAGAAAGTGCACAGAAAGTGT 1193
QY 381 ***IleAsnGly***Val***ProGlnGlyValAlaLeu*****PheAsnValTrpGlnVal 400
Db GAGATTAAATGATATGTGATCCCAAGGAGGAGCATTTGATCTTCAATATATGGCAAGTA 1253
QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGlnArgPheLeuGln 420
Db GGAAGAGACCCCAATACAGGAGACAGACATGAGATTCGCTCGTAGAGGTTCTTAGAG 1313
QY 421 Thr***AlaGlyGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db ACAGGGGCTGAAGGGGAGACAGGCGCTTGTGATCTTAAGGGGACAAATTTCAACTTCTC 1373
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
Db CCAATTGGGTCTGGAGGAGAAATGTGCTCGAGATCAATCTGCTACTTCGGGAATGGCA 1433
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGln 480
Db ACACTTCTTGCACTCTTATTCAGTGTCTCGACTTGAAGTGTGGGTCCACAAGAGACAG 1493
QY 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
Db ATATTGAAGGGTGTGACCCCAAGTTAGCATGAAAGAGAGAGCCGCTCACTGTTCACA 1553
QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
Db AAGGACATATGCTTGTGTGTGTCTTCACTTGCAAGGATCGGCGTTCATCTAACTCTT 1613
QY 521 Ser 521
Db 1614 TCT 1616
RESULT 2
US-09-672-785-3
Sequence 3, Application US/09672785
Patent No. 6596927
GENERAL INFORMATION:
APPLICANT: Mizutani, Masako
APPLICANT: Kasumi, Takaaki
APPLICANT: Ayabe, Shin-ichi
APPLICANT: Akashi, Tomoyoshi
TITLE OF INVENTION: Genes Coding for Flavone Synthases
FILE REFERENCE: 001560-183
CURRENT APPLICATION NUMBER: US/09/672,785
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP00/04379
PRIOR FILING DATE: 2000-01-30


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; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-09-672-785-1

Alignment Scores:
Pred. No.: 7,24e-120 Length: 1724
Score: 943.50 Matches: 198
Percent Similarity: 57.31% Conservative: 88
Best Local Similarity: 39.68% Mismatches: 179
Query Match: 39.49% Indels: 34
DB: 3 Gaps: 9

US-09-857-581b-66 (1-521) x US-09-672-785-1 (1-1724)

QY 33 ProAnProProSerPro***Pro-Arg-----LeuPr 43
DB 87 CTTCAACCTCTTCAACCCGCGCGCAAGACCCGCCGCCGCCCTTACCTCC 146
QY 43 oPhelleglyHs***HisLeuLeuLysAspLysLeuHisLysAla***IleAspLe 63
DB 147 CTTAATAGGCCACTTACACTCTCTCGCCCAAG---CTCCACACACCTTCACCAATT 203
QY 63 uSerLysLysHsLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 83
DB 204 CTCACACGCTACGCGCGCGCTCATCAGCTCTACCTCGCTCGCTCGCTCGCTCGCT 263
QY 83 aSerThrProGluLeuPheLysLeuPheLysLeuGln*****GluAlaThrSerPhe***Th 103
DB 264 TTCACACGCGCGCAACTCGCGCGCAATTCTTCAAGACGACGAA--CTGACATCTTCGCT 320
QY 103 rArgPheGlnThrSerAla***Arg***LeuThrLysAsp*****ValAla*****Pr 123
DB 321 CCGCAAGCACTCCACCGCGCATGACATGCGACGTACGACTCTCGTGGCTTCGCGCGC 380
QY 123 o***GlyProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 143
DB 381 GTACGCGCGCGTACTGGAATTCATCAAGAAATTAATGACTTACGAGCTACTGGGTCGCG 440
QY 143 rThrValAsn***LeuArgProLeuArgThrGlnGlnLysLysLysLysLysLysLys 163
DB 441 GAACCTTGACCACTTCACGCCCTTAGAGCTTGGAGTCACACAGTTTCTTGAAATTTT 500
QY 163 rAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLysLeuLysLysLys 183
DB 501 GTACGGAAGAAACAGACAGAAACAGAGCTTAAATGACTGACGAGAGCTTGTAAAGCTGAC 560
QY 183 *AsnSerThr***SerMetMet***Leu-----GlyGluAla 195
DB 561 GAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
QY 195 aGluGluLysLeuArgLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 215
DB 621 GGAGGTGGCGAGGACCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680
QY 215 rAspPheLys***ProLeuLys***LeuLysValGlyLysLysLysLysLysLysLysLys 235
DB 681 GGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 740
QY 235 rIleLeuAsnLysPheAspProValAlaGluArgValLysLysLysLysLysLysLysLys 255
DB 1553 CGGGTTCAGGCTCCACGTCGCAATGATTTGGTGTCCCAATTGGTCCACGGAATT 1553
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DB 741 TATTAGGAGAGGTATGATGCTTTGTTGGAGAGATTAATTAGTATGAGGAGGTG-- 798
QY 255 lArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAspTh 275
DB 799 -AGGTTCAGGCGGGGTGTTGTTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 854
QY 275 rLeuLeuGluPheAlaGluAspGluThr***GluLysLysLysLysLysLysLysLysLys 295
DB 855 GTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 914
QY 295 *GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThGluTr 315
DB 915 ACCTTGAATTCGAGATTTCTTCACTGCGGTACACACACACACACACACACACACACAA 974
QY 315 rAlaLeuAlaGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 335
DB 975 GGCAATGACGAGAACTCATTTAGCAATTCATATCTACTCAAAAAGCTCAAGAAAGAGTGA 1034
QY 335 rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrTl 355
DB 1035 CAAAGTCATAGATCAACAAGGTTGTGCAAGATCCGACGCGCCCTTAATTCCTTACCT 1094
QY 355 eArgAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 375
DB 1095 CAACGATCATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1154
QY 375 eCys***GluGlyCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Ph 395
DB 1155 ATCAATTTCTGACGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1214
QY 395 eAsnValTyrGlnValGly***Asp***LysTyrTyrAspArgProSerGlu***ArgPr 415
DB 1215 CAACCTTGTGTCATGAGGAAGAAATCTTAATCTGAGGAATCCGATGAGTCCGAC 1274
QY 415 oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgLys 435
DB 1275 CGAGAGGTTTCTCGAAGAGG-----ACCGGTGATGATGATGATGATGATGATGATG 1322
QY 435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl 455
DB 1323 GCAATTCAGTTGCTGCGCTTTGGACAGGCGCGCGCGCGCTCGCGGAGATGTTGAG 1382
QY 455 aThrSerGly***AlaThrLeuAlaSerLeuLysGlnCysPheAspLeuGlnValLe 475
DB 1383 CATGACAGGTTGTTAGATTAATGCGGGCTATGAGTGTGCTGCTTCAATTGAAACTG-- 1440
QY 475 uGlyProGlnGlyGlnLysLeuLysGly***AspAlaLysValSerMetGluGluArgL 495
DB 1441 ---CCCGATGATG-------AAGTCGTCGACATGACCGAGCGGCC 1478
QY 495 aGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgLle 513
DB 1479 CGGGTTCAGGCTCCACGTCGCAATGATTTGGTGTCCCAATTGGTCCACGGAATT 1553

RESULT 4
US-09-672-785-7
; Sequence 7, Application US/09672785
; Patent No. 6536927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
```

PRIOR APPLICATION NUMBER: JP 11-22427
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 7
 LENGTH: 1770
 TYPE: DNA
 ORGANISM: *Perilla frutescens*
 FEATURE:
 OTHER INFORMATION: Nucleotide sequence encoding a protein having an activity to directly convert flavanone to flavone
 US-09-672-785-7

Alignment Scores:

Pred. No.:	8,35e-117	Length:	1770
Score:	921.50	Matches:	190
Percent Similarity:	57.46%	Conservative:	91
Best Local Similarity:	38.85%	Mismatches:	183
Query Match:	38.57%	Indels:	25
		Gaps:	8

US-09-857-581b-66 (1-521) x US-09-672-785-7 (1-1770)

QY ProAspProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLys 52
 DB CCTACCTCCCGGGCGTCCCT---CTCCCATCATCGGCCACCTTACCTCTCGG 155
 QY AspLeuLeuHisTyrAla***LeuAspLeuSerLysHisGlyProLeuPheSer 72
 DB CCGAGA---CTCCACCAACCTTCCACGATCTGCTCCACAGGTAACGGCCCTTAATGAC 212
 QY *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysPhe 92
 DB CTCGGCCTCGGGTCATCCCTCGCTGCTATCTGCTCCGCGAGCTCGCCAGGAATGC 272
 QY LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg** 112
 DB CTCAAGACACAGAGCTCGTC---TTCCTCCCGCGAACAACCTCACCGCATGATATC 329
 QY LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheValArg 132
 DB GTCACTGATTCATCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 389
 QY LysLeuLeuLeuMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArg 152
 DB AAATTAATGACCTACGAGCTGCTCGGGCCGGAATCTCGCCCATTCACCCATGACG 449
 QY ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysPro 172
 DB ACTCTCAAGTCAAGTCTTCTCTCAATCTTATGCGCAAGGTGAATCGGGGAGAGC 509
 QY LeuAsp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu 192
 DB TTCAACGTGACTGAGAGCTGCTGTAAGCTGACGAGCAACGTCAATATGCAATATGCTG 569
 QY -----GluGluAlaGluGluIleArgAspIleAlaArgGlu 204
 DB AGCATACGCTGTTACAGACGAGTCCGAGCGGAGGCGGAGAGACCGTATTCGGGAG 629
 QY ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
 DB GTCAAGCATATTTGGGAGTTCAGAGCTCCGACATCATATGCTTGAAGAATCTC 689
 QY LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValVal 244
 DB GATTTCACAGGTATTAAGAGCGGTCCGAGATATCCAGAGATATGATGCTCTGCTG 749
 QY GluArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu***** 264
 DB GAGAGATATCATCCGACAGAGAGAG---CAGAGCGGAGCCACCGCGCGCTGCG 803
 QY GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr 284

DB GGCGCGGGGAGCCAGGATTTCTTACATGTTCTCTGACATATGAGAGCGGAGAA 863
 QY ***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAla 304
 DB GCCAGATTAATTCACGAGGAGGATCTCAAGGCTTATCTGATTTCTTACCGCCG 923
 QY Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro 324
 DB GGACCCGACACAGCGCGATCTGTGTGATGGGCGATGACGAGACTATCAACATCC 983
 QY ***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuVal 344
 DB AATGTGTTAAGAAAGCTCAAGAGAGATGGCAATCTGTGGATTCACAGAAATCTG 1043
 QY AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
 DB CAAGATTCGAGCGCCCAATCTGCTCTTCAACCTTCATCAAGAACATTCGCG 1103
 QY MetHisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly 384
 DB CTCACCTCTCAATCCCAATGCTGGCGAGAAATCGATCTCGACTGCTCATCGAGC 1163
 QY ***Val***ProGluGluValLeu*****PheAsnValTrpGluValGly***Asp*** 404
 DB TACATATTCGCGCAACGCTGCTCTTCTGTCACCTGTGTCATGGGCGGAACCT 1223
 QY LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGlu 424
 DB AAATCTGGGACTACCGGAGCGGCTTCACGCGGAGAGGTTCTCGAGAAAG----- 1274
 QY GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
 DB ---GAAAGGCCCGCATCGATGTGTAAGGCGACATTTGAGCTGCTACCGTTGGAAGC 1331
 QY GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
 DB GGAGAGAGAGCTGCGCCAGGAGTCTTTAGCATTCAGAGGTGTCATCAATATGCG 1391
 QY SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
 DB AGCATATTCATGCTTCGATGGAAGCTG-----CCGACGCG----- 1430
 QY ***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
 DB ---TCCGGCCATGTGATATGCGAGAACCGCGCGCTCAGGACCGGAGAGACCGAT 1487
 QY LeuValCysValProLeuAlaArgIle 513
 DB TTGTTTGGCGGTGTGTCGCGAGATT 1514

RESULT 5
 US-09-142-108C-16
 Sequence 16, Application US/09142108C
 Patent No. 6774285
 GENERAL INFORMATION:
 APPLICANT: Brugnolera, Filippa
 APPLICANT: Holton, Timothy A.
 APPLICANT: Michael, Michael Z.
 TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
 TITLE OF INVENTION: AND USES THEREFOR
 FILE REFERENCE: 11658
 CURRENT APPLICATION NUMBER: US/09/142,108C
 PRIOR FILING DATE: 1998-09-01
 PRIOR APPLICATION NUMBER: P8386
 PRIOR FILING DATE: 1996-03-01
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 16
 LENGTH: 1660
 TYPE: DNA
 ORGANISM: *Chrysanthemum*
 FEATURE:
 NAME/KEY: CDS


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Query Match: 26.33% Indels: 44
DB: 3 Gaps: 12

US-09-857-581B-66 (1-521) x US-09-689-783A-1 (1-1488)

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 106 CCACGAGGCCAAMACCA---TGGCCCATTAATGGAAGAACTTCAACTTATTT---GGAACC 159
QY 55 LeuLeuIleTyAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
DB 160 CTCGCCACACCAATCCCTCCATGAGGCTCACCCAAAATATGACATTAATGACATCATG 219
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
DB 220 TTTCGGCTCCAAAGCGTCGTCGTCGCTCACTGTGAATATGGCGAAACCTTTCTCAAA 279
QY 95 *****GluAlaIleThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 280 ACCCAGCAGCAACG---TTAGCCGGCCGACCCCAATTTCTGCGGAAAATACACAACT 336
QY 115 TyrAsp-----ValAlaAla*****Pro***GlyProTyrTrp***PheValArgLys 133
DB 337 TATTACTACTGACATTAACCTTGTGCTCACTACGCTCCGATTTGGCGCCAAAGCTCGGAGA 396
QY 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
DB 397 ATGTGCTATTAATGATTTTGTAGTGCAAAACGCTTGAGCTTATGATGATCAATTAAGAAA 456
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
DB 457 CAAGAGTTACATGTTTTCATGACATGAACCTTTGATTTCTGAAC---AAACAACTT 510
QY 174 Asp***ThrGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
DB 511 TTGTTGAAGACCATTTTCAAGTTTGATGCTTAAGTTTAAGTAAAGATGGCTTAAAGA 570
QY 194 -----GluAlaGluGluIleArgAspIle 201
DB 571 AGGAATATCTAGAGAGTTGAAATTTCTATTATTTCTCCGATGATGTTTAAGAAATATG 630
QY 202 AlaArgGluValLeuLysIle***GlyGlnTyrSerLeuThrAspPheIle***ProLeu 221
DB 631 TTGGATGAGTGTGTTTCTTAATGCGATTTCTTAATTTGGGAGATTTTATTTCTTGAT 690
QY 222 Lys***LeuLysValGlyLysTyrGluLysArgLysAspIleLeuAsnLysPheAsp 241
DB 691 CATTTCTTAGATTTTCAAGGATATGTGAAGAGATGAAGTTTGAAGTAAAGATTTGAT 750
QY 242 ProValValGluArgValIleLysLysArgArg***IleValAlaArgArg***AsnGly 261
DB 751 GGATTTATGGAACATGTGTTGAGGAACAT-----ATTGAAGAAAGAAAAGCTTTAAG 804
QY 262 Glu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGlu 281
DB 805 GATTAATGTGCTAGAT-----ATGGTGAATGTTCTTTGCAACTTGCTGAG 852
QY 282 AspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp*** 301
DB 853 GATCTGATCTTTGAAGTCMAACTTGAAACATGATGATGTTAAAGCTTTTACTCAGACCTG 912
QY 302 PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIle 321
DB 913 ATACGAGGAGGACAGAGAGCTCAGACATGACATGATGGCAATCTCAGACTATA 972
QY 322 AsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerValValGlyLysAsp 341
DB 973 AGAAACACCAAAATCTTCAGAAAGCAACAGAGCAATCTGACAGATATGAGAGAGAA 1032
QY 342 ***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGlu 361
DB 1033 AGATGGTTGAAGAGAAAGACATTTGCTATCTTATGTTATGCAATTTGCTTAAGAA 1092

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QY 362 ThrPheArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys 380
DB 1093 ACAATGACATCTTCAACCCAGTGGACCAATGTTAGTACCAAGAGAGCTTAAGAGATTGC 1152
QY 381 ***IleAsnGly***Val***ProGluGluValAlaLeu*****PheAsnValTrpGlnVal 400
DB 1153 AATATCAATGATATGATATGATTTCCAAAGAGCTTTGATTTCTTTTAATTAATCTTGAGCAATT 1212
QY 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGln 420
DB 1213 GCAGAGATTTTAATGTTTGGATATATCAATATGAGTTTATGCCAGAGAGTTTCTT--- 1269
QY 421 Thr***AlaGluGluValAla*****LeuAspLeuArgLys***HisPheGlnLeuLeu 440
DB 1270 -----GTAAGATATATGATGTAAGAGCAATGATTAATGATTTGTTG 1311
QY 441 PropheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1312 CCATTTGGTGTGTGAAGAAATGTGTCTGCTTACCTTGTGATTAAGGTTAATTCAA 1371
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
DB 1372 TCAAGTTTGGCTTAATTTGTTGATGATGATTTAATGAGATTTG--- 1413
QY 481 IleLeuLysGly***AspAlaLys-----ValSerMetGluGluValArgAlaGlyLeu 497
DB 1414 -----AGTATGATGATGAAAGAAAGCAATTTGAATATGAGAGATTTTGGGCTT 1464
QY 498 ThrValProArg 501
DB 1465 TCTACACCTAAG 1476

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RESULT 7
US-09-142-108C-5
; Sequence 5, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
; APPLICANT: Bruggliera, Filippa
; APPLICANT: Holton, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/09/142,108C
; CURRENT FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: PNB386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1711
; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (91)..(1629)
; US-09-142-108C-5

Alignment Scores:
Pred. No.: 6,12e-76
Score: 626.00
Percent Similarity: 47.94%
Best Local Similarity: 30.34%
Query Match: 26.20%
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-142-108C-5 (1-1711)

QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 145 TTATTTGGTCCATGATCTTTTAATTAATGAGGTTCTTCTTATATATCTTCTCTC----- 198
QY 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40

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Db 199 -----ACAAAAAGTAAGCCACCTGCGACCGAAGCATGGCCC 243
Qy 41 -----ArgLeuProPheIleGlyHis**HisLeuLeuLysAspLysLeuLeuHis 57
Db 244 ATCGTCGGAATTCGGACATCTTGGCGGAAAGCCC-----CAC 282
Qy 58 TyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySer 77
Db 283 CAGTCGATGGCGGCGCTGGACGGGTGACGGCCCAATTAATCATCTGAAGATGGGCTTT 342
Qy 78 MetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****Glu 97
Db 343 GTGCATGTGTGTGTGGCTCTCCAGCATCCGTTGGCGAAGAAATTTCTGAAGGTCATGAC 402
Qy 98 AlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp--- 116
Db 403 GCA---AATCTTCGACAGGCGCTCCCAATTCGGGTGCAAAACACGTGGCTTACACATAT 459
Qy 117 *****ValAla*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMet 136
Db 460 CAGGACTGTGCTTCTCTCTTATGGCCACGCTGGCGATGCTCAGAAATCTGTGCA 519
Qy 137 AsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIle 156
Db 520 CTCACCTCTCTTCCGCGCAAGCCTTGAACGACTTCACACAGTCAGACGATGAGTG 579
Qy 157 ArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***Thr 176
Db 580 GGGATCCTCACTCGCTTCTAGCAGATGACAGAAACG-----CCGTGAATATGAGG 633
Qy 177 GluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly----- 193
Db 634 CAGATATGAACATGACGCGCCACCAATGCAATGCGGTGTATGTTGGTCAACCGGTG 693
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLys 207
Db 694 GTTGCACAGCAGACTCAAAAGCGGAGGAGTTTAAGGCAATGATGAGGATGATGATG 753
Qy 208 Ile***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 754 TTAGCTGTGTGTCACTTAGGTGATTTATTCACCTCTTAAATAATGATGATCTTCA 813
Qy 225 -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
Db 814 GGTGTATTGCTAAGATGAAGAAGCTTCACTTGCATTCGATTCCTTGAAGTAAAG--- 870
Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db 871 -----ATCCTGGAGACCAAGATC 891
Qy 261 GlyGlu*****GluGlyGlu**SerGlyVal**LeuAspThrLeuLeuGluPheAla 280
Db 892 AACAGCTCAGATGAACCAAAAGGCCATTCGATTTGTGTAACATGTTAATTTCTTGAAG 951
Qy 281 Glu---AspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValAla 299
Db 952 GAGCGCTGATGATCCCAAGAGGAGGAGCTACCGACGTGAATTAAGCGTTCCTTGG 1011
Qy 300 Asp***PheSerAlaGly**AspSerThrAla*****ThrGluTrpAlaLeuAlaGlu 319
Db 1012 AACTGTTTGTCTGACAGAACTGACACACATCAAGACCTGTGAATGTGTCATAGCTGAG 1071
Qy 320 LeuIleAsnAsnPro**ValLeu*****AlaArgGluGlu**TyrSerValValGly 339
Db 1072 TTAGTACGACATCTTAATCTTGGCCCAAGTCCAAATAAATCTGACTCTGTGTGTGG 1131
Qy 340 LysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleVal 359
Db 1132 AAGAATCGGTGTGAAGAGGCTGATCTGGCCGATATCAATTCCTCCAAAGCGGTGTC 1191
Qy 360 LysGluThrPheArgMetHisProProLeuProVal---ValLysArgLysCys***Glu 378

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Db 1192 AAGAAATTTCCGACTCCATCCCTTCAACCCCGCTCTCCCTACCGAGATCCGACATGAG 1251
Qy 379 GlyCys***IleAsnGly***Val***ProGluGluValAlaLeu*****PheAsnValTrp 398
Db 1252 AATTGTGAAGTGAATGAATGATCTGATTCCTAAAGGGTTCACACTTCTTGTCAATGTTGG 1311
Qy 399 GluValGly**Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPhe 418
Db 1312 GCAATTTGCTCGGAGATCCAAATGTGTGGATGAACCATGAGATTCCTCGGCTGAACGATTC 1371
Qy 419 LeuGluThr**AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGln 438
Db 1372 TTGAAG-----GGCGGGGAAAAGCCTTAATGTGAGTGTAGAGGATGATTTGCA 1422
Qy 439 LeuLeuProPheGlySerGlyArg**MetCysProGluVal**LeuAlaThrSerGly 458
Db 1423 TTGATTCGTTGTGAGCGGGCGGAAAGATTTGTGAGAGATAGCTTGAATACCTATG 1482
Qy 459 **AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGluValLeuGlyProGln 478
Db 1483 GTCCAGTTGTTGACAGCAACTTGAACCATGCGTTGACTTGATTTG-----GGCGAT 1536
Qy 479 GlyGluIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThr 498
Db 1537 GGAACAGTTG-----CCTGAAGACTTAAACATGAGAGAAAGCTTATGCGCTGACC 1584
Qy 499 ValProArgAlaHisSerLeuValCysValProLeuAlaArg 512
Db 1585 TTGCACAGAGCTGACCTTGGTGAATGACCCGAAAGCCTTAGG 1626

RESULT 8
US-09-499-302A-1
/ Sequence 1. Application US/09499302A
/ Patent No. 6369212
/ GENERAL INFORMATION:
/ APPLICANT: BOUNG-JUN, OH
/ APPLICANT: MOON, KYUNG KO
/ APPLICANT: YOUNG, SOON KIM
/ TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
/ TITLE OF INVENTION: INCOMPATIBLE INTERACTION
/ FILE REFERENCE: 10324/P6443050
/ CURRENT APPLICATION NUMBER: US/09/499,302A
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1781
/ TYPE: DNA
/ ORGANISM: Capsicum annum
US-09-499-302A-1

Alignment Scores:
Pred. No.: 8.95e-76 Length: 1781
Score: 625.00 Matches: 151
Percent Similarity: 49.28 Conservative: 89
Best Local Similarity: 31.01 Mismatches: 211
Query Match: 26.16 Indels: 35
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-499-302A-1 (1-1781)
Qy 35 ProProSerPro**ProArgLeuProPheIleGlyHis**HisLeuLeu-----Lys 52
Db 100 CTCCTCGTCCATGCG---AAATTAACCTTTATTTGAAGCCTACATCACTTGGCAGTGGCA 156
Qy 53 AspLysLeuLeuHisTyrAla**IleAspLeuSerLysLysHisGlyProLeuPheSer 72
Db 157 GGTTCACCTTCCTCATATGAGCGCTAAATAAATCTAGCAAACTTATGAGCGCGCTCATGAC 216
Qy 73 ****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysPhe 92
Db 217 TTACGACTGGGGAATTTCTACCGTCATCATTTGTGTCCTCCGCGAATGCGAAGAAATA 276

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Qy      93 LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
      277 CTRAAACACGACGAC---CTCGCTTCGCAAGAGCCGCAAACTGTGTGCTGCATC 333
Qy      113 LeuThrTyAsp*****ValAla*****Pro***GlyProTyrTrp***PheVal 131
      334 GTCCATTATGATAGTACGATATAGCATTTTCTCATGTGTGTAATATCTGAGCGAGATT 393
Qy      132 ArgGlyLeuLeuLeuSerAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeu 151
      394 CGTAAATTTGGCACTCGACTCGACTCTTATGTGCAAGATGTCCAATTTCTTATGCTCAAT 453
Db      152 ArgThrGlnGlnLeuArg-----Lys***LeuArg***NerAlaGln***AlaGln 168
      454 CGCCAGAGTAGAGTGTGATGATGATGCTCATCTATACGAACATGCAATTTT----- 507
Qy      169 Ala***LysProLeuAsp***ThrGluGluLeuLeuLysTrp***AsnSerThr***Ser 188
      508 -----CCCGTCAACCTTACAGACAAATATTTTGGTTTCAAGTTTCGTACTGTGT 558
Qy      189 MetMet***LeuGly-----GluAlaGluGluLeuArgAspIleAlaArgGlu 204
      559 AGATCAGCTCTGGGAAAAATATGTCTGTACCAAGCAAACTGTAATTTTCATGAGGAA 618
Db      205 ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224
      619 ATATATCATGTACGAGTGTGATTTAGTATGCTGATTTTCCCTCATAGGAAATGCTTA 678
Qy      225 ---LysValGlyLysTyrGluLysArgIleAspAspIleLeuLysPheAspProVal 243
      679 CATGATGTGTGTTGTTCAAAACTAGACTGCTGAGGCTCATGTAAATTCATGATGATT 728
Qy      244 ValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu 263
      739 TTGGACATGTAGTATGATGAGACAA-----CAGATGAGCGGATGGCAAAAG 789
Db      264 ***GluGlyGlu***SerGlyVal**Leu---AspThrLeuLeuGluPheAlaGluAsp 282
      790 GGTATATGCGAATTTGGCGGTGAAGATTGATGATGCTTTTGTCAAGGTTGCGAAAGT 849
Qy      283 GluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***Phe 302
      850 GGAAGATGTCAAATTTCCATCACGATGACAAATTCAAATCAATATTAAGTGAATGCTTC 909
Qy      303 SerIleGly***AspSerThrAla*****ThrGluThrAlaLeuAlaGluLeuIleAsn 322
      910 TCCGCTGATCTGTAAGCGTATCGATCACTAATAATTTGGGATTAAGCTGAATATGAAAG 969
Db      323 AsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp*** 342
      970 AAACCAAGTGTTCATGCAAGGACCAAGCTGAAGTGAAGCAAGCTTGAAGGAAAGAA 1029
Qy      343 LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThr 362
      1030 GGTTCACAAATATGATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1089
Qy      363 PheArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys*** 381
      1090 CTAAAGATGACACCTCCCAATTCCTATTAATGCTCTAGAGATATGCAAGATPACAAG 1149
Db      382 IleAsnGly***Val***ProGluGlyValAlaLeu*****PheAsnValTyrGlnValGly 401
      1150 ATTACCGGTACATATATCTTCAAACTCGAATCATATGTAATGATGCGCAATTCGA 1209
Qy      402 ***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr 421
      1210 CGAGATCTCTGAAAGTTGGATGACCTTGAAGCTTTTCCAGAGAGATTC----- 1260
Db      422 ***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuPro 441
      1261 -----GAGCAATAGTTCTTGTGATCTTCTTGGAAGCATCATCATTTATTCGA 1308
Qy      442 PheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThr 461

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Db      1309 TTTGGTGGGGAAGAGATTTGTCTCGAATGCTTTTGTGTTAGCCAAATGTGAGCA 1368
Qy      462 LeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyIle 481
      1369 CCATTATGCTCATTTACTTTATCATCTTCATCGAAGAACTC-----CTTAATGCAAAAGT 1422
Qy      482 LeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArg 501
      1423 CACGAAATTTTGGAC-----ATGACGAGATGACCTGGAATTTCTGCAACAAAGA 1470
Db      502 AlaHisSerLeuValCysVal 508
      1471 AAGGATGATCTTGTGTTGATT 1491

RESULT 9
US-09-142-108C-14
/ Sequence 14, Application US/09142108C
/ Patent No. 6774285
/ GENERAL INFORMATION:
/ APPLICANT: Bruggliera, Filippa
/ APPLICANT: Holton, Timothy A.
/ APPLICANT: Michael, Michael Z.
/ TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
/ TITLE OF INVENTION: AND USES THEREFOR
/ FILE REFERENCE: 11658
/ CURRENT APPLICATION NUMBER: US/09/142,108C
/ PRIOR FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: PN8386
/ PRIOR FILING DATE: 1996-03-01
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 1748
/ TYPE: DNA
/ ORGANISM: Rosa hybrida
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (22)..(1563)
US-09-142-108C-14

Alignment Scores:
Pred. No.: 1,64e-75 Length: 1748
Score: 623.00 Matches: 161
Percent Similarity: 48.73% Conservative: 89
Best Local Similarity: 31.38% Mismatches: 205
Query Match: 26.08% Indels: 58
DB: Gaps: 16

US-09-857-581B-66 (1-521) x US-09-142-108C-14 (1-1748)
Qy      27 LysAlaLeuArgHis---LeuProAsnProProSerPro***ProArgLeuProPheIle 45
      88 AAATCCCAACGACCACTCGCTCTCTCCCTCGGCCCAACCA---TGGCCGGTGT 144
Qy      46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSer 64
      145 GGCACCTTACCTCACTG-----GGCCCTTCCCGGACCACTCAATCGCGAGTTGGCG 198
Qy      65 LysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValValAlaSer 84
      199 AAGAAACACGGCGCGCTCATGACCTCGGCTGCTAGCTGATGATGATGATGATGATGATG 258
Db      85 ThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArg 104
      259 TCAAGATCGGTAGAGGCGCCAGTTCTTGAAGATCAAGACGCC--AATTTCTCAGCGCA 315
Qy      105 PheGlnThrSerAla***Arg***LeuThrTyAsp---*****ValAla*****Pro 123
      316 CCGCCCACTCTCGCGCCGCAACCTGCTATTAATCAAGACGACCTCTGTTTCAGGCG 375
Qy      124 ***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThr 143

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Db 376 TACGGTCACGGTGGCGCATGTTCCGAAAGATCAGCTCCGTCATCTGTTCCGGCAAA 435
 QY 144 ThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***Met 163
 Db 436 GCGTTGGATGATCTTAAACACGTCGCGAGAGAGAGTAAGTGTGCTGACGCGATGCTTG 495
 QY 164 AlaGln***AlaGlnIle***LysProLeuAsp***ThrGlnIleLeuLeuLysTrp*** 183
 Db 496 GCAAAAT-----TCAGGGTCAAAGGTAAGTGAACCTGGCGCAACTGCTGAACCTGTCAAG 549
 QY 184 AsnSerThr***SerMetMet***LeuGly----- 193
 Db 550 GTCAATGCTCTAGAAAGGTGAGTGAAGCGGAGGTTTTCGCGACGCGACGCGAGGC 609
 QY 194 -----GlnAlaGlnIleArgAspIleAlaArgGlnValLeuLysIle***Gly 210
 Db 610 GACGATCCGAGCGGACGGAGTTCAATGATGATGATGATGATGATGATGATGATGATGATG 669
 QY 211 GlnTrpSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
 Db 670 GGTTCACATAGTGTGACTTCATCCCTCTCTGAAATGCTTGACCTTGCAAGCGGTGGCG 729
 QY 225 ---LysValGlyLysTrpGlnLysArgIleAspAspIleLeuAsnLysPheAspProVal 243
 Db 730 TCCAGATGAAGAGGTCCACAGAGATTCGACGACTTCTTGAACA----- 774
 QY 244 ValGlnArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu*** 263
 Db 775 -----GCCATTGTGAGAGACCAAGAAAGGCTCCGCG 807
 QY 264 ***GlnGlyGlu***SerGlyVal***LeuAspThrLeuLeuGlnPheAlaGlnAspGln 283
 Db 808 ACGCGCGGCGACGCTCAC-----ATGTTGACCACTCTGCTCGCTCAAGAGAGCGCGC 861
 QY 284 Thr***Glu---IleLysIleThrLys***Ile***GlyLeuValValAsp***Phe 302
 Db 862 GACGGGGAAGAGGAGGAGCTCACCGATCTGAATCAAAAGCTTGTGTTGAACAGTTC 921
 QY 303 SerAlaGly***AspSerThrAla*****ThrGlnTrpAlaLeuAlaGlnLeuIleAsn 322
 Db 922 ACGGCTGGACCTGATACGTCATGACGACGCGTGGAAATGGGCAATAGCTGAATCTATTCG 961
 QY 323 AsnPro***ValLeu*****AlaArgGlnGlu***TyrSerValValGlyLysAsp*** 342
 Db 982 CACCTCATATGCTTAGCGGCGAGTTCAAGAAAGCTTGACATTTGTGGCCATGACCGA 1041
 QY 343 LeuValAspGlnValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGlnLys 362
 Db 1042 CTTGTGACCGAATCCGACATACCCAACTCCCTTACTCCAAAGCTGATCAAGAGAAACG 1101
 QY 363 PheArgMetHisProProLeuProVal---ValLysArgLysCys***GlnGluCys*** 381
 Db 1102 TTCGAGCTCCACCACTCCACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
 QY 382 IleAsnGly***Val***ProGlnGlyAlaLeu*****PheAsnValTrpGlnValGly 401
 Db 1162 ATCAACGGGTACACATCCGAAAGGCTCCACACTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1221
 QY 402 ***Asp***LysTrpTrpAspArgProSerGln***ArgProGlnArgPheLeuGlnLys 421
 Db 1222 CGTGACCCGCGTAATGGCGCGACCACTGAGTTCAAGCCCGAGAGGTTCTCGT----- 1275
 QY 422 ***AlaGlnGlyGlnIle*****LeuAspLeuArgGly***HisPheGlnLeuLeuPro 441
 Db 1276 ---CCGGGGGGGCAAAAGCTTAATGTTGATATTAGAGAAACGATTTTGAAGTCATPACC 1332
 QY 442 PheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThr 461
 Db 1333 TTGGGTGCGCGGAGAAATATGTCGCGGATGAGCTTGGGCTCGCTGATGCTCATTTA 1392
 QY 462 LeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIle 481
 Db 1393 ATGACTGCAACATTTGTCACGCACTTAAT-----TGGGCGCTTG 1431

QY 482 LeuLysGly***AspAla---LysValSerMetGlnGlnArgAlaGlyLeuThrValPro 500
 Db 1432 GGTGATGGGCTGACCGCTGAGAAAGTTAAACATGATGAAGCATATGGGCTCACTCAACA 1491
 QY 501 ArgAlaHisSerLeuValCysValProLeuAlaIleGlyIle 513
 Db 1492 CGAGCTGACCGCTTAATGTTGTCACCGCGCACAGGCTTG 1530
 RESULT 10
 US-08-881-784-5
 ; Sequence 5, Application US/08881784
 ; Patent No. 6083731
 ; GENERAL INFORMATION:
 ; APPLICANT: Croteau, Rodney B.
 ; APPLICANT: Lupien, Shari L.
 ; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Christensen, O'Connor, Johnson and Kindness
 ; STREET: 1420 Fifth Avenue, Suite 2800
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/881,784
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Shelton, Dennis K.
 ; REGISTRATION NUMBER: 26,997
 ; REFERENCE/DOCKET NUMBER: WSUR19777
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 224-0718
 ; TELEFAX: (206) 224-0779
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1762 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mentha spicata
 ; INDIVIDUAL ISOLATE: cDNA encoding
 ; IMMEDIATE SOURCE:
 ; CLONE: pSM12.2
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 558..1212
 ; OTHER INFORMATION: /product= "Probe LH-1 (Figure 4A)"
 ; NAME/KEY: misc_feature
 ; LOCATION: 39..538
 ; OTHER INFORMATION: /product= "Probe LH-2 (Figure 4A)"
 ; US-08-881-784-5
 Alignment Scores:
 Pred. No.: 6,98e-75 Length: 1762
 Score: 618.50 Matches: 146
 Percent Similarity: 48.38 Conservative: 93
 Best Local Similarity: 29.55 Mismatches: 214
 Query Match: 25.89 Indels: 41


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Db      152 GGCACCTCCACTTCTGTGGGAGGCGTTCCCCAGACGTTTGAAGACATAGCCCAAG 211
Qy      66 IYSHLEGLYProleuPheSer*****PheGLYSerMetProThyValValAlaSerThr 85
Db      212 AAGTACGGGCGCGGTGGCGACGTCGACCTGGGAGAGATGATCCTGGGTGGTGTGTGTG 271
Qy      86 ProGLYleuPheleuGLY*****GLAlaThrSerPhe***ThrArgPhe 105
Db      272 GGGGAGGACCGAAGACGCGATGAAGGCTCTGAC---CCGAACCTCCCGACCGGCTTC 328
Qy      106 GlnThrSerAla***Arg***LeuThrTyraSP-----ValAla*****Pro*** 124
Db      329 GACGGCATCGGGTCCAGACCATGTGATACGAAGAATGACATCTTCACCGCTTAC 388
Qy      125 GlyProTyTrp***PheValArglySleuIleMetAsnAspLeu***AsnAlaThrThr 144
Db      389 AACGATCCTGGCGGACGATGCGAGAGATCTGCGTACAGAGCTGTGAGCCCGAAGAAC 448
Qy      145 ValAsn***LeuArgProleuArgThrGlnGlnIleArglys***LeuArg***MetAla 164
Db      449 GTCCAGTCTCTCGGATACATAGGACAGAGAGATGACGGCTTCATCCGGTCTCGGG 508
Qy      165 Gln***AlaGluAla***LysProleuAsp***ThrGlnIleuLeuLysTrp***Asn 184
Db      509 TCGTCGGGGAGAGCG-----CCGTGACGTCGACGAGAGAGGTGTGAAAGATGTGTGT 562
Qy      185 SerThr***SerMetMet***LeuGly-----GluAlaGlnGlnIleArgAsp 200
Db      563 GTCTGTGTGTGACGGCGCGGCTTCGGGAGTGTCTCAAGAACGACGAGTTCGTTGGCGAG 622
Qy      201 IleAlaArgGluValIleuLysIle***GlyLysTrpSerLeuThrAspPheIle***Pro 220
Db      623 TTGGTAAAGAGATCGCTGGCATTTGGCGTCCGGGTTTGGTGGCGGAT---CTCTACCT 679
Qy      221 -----LeuLys***LeuLysValGlyLysTrpGlnLysArgIleAspPheIle 236
Db      680 TCCTCATGGCTCTCAACCTGCTTAGCTTGAACAAGTAC-----AGTTGACAGAGATG 723
Qy      237 LeuAsnLysPheAspProValIleGluArgValIleLysLysArgTrp***IleValArg 256
Db      734 CGCGCGCGCTCATACATCTTGATGGGTTCTCTGAGAGGATGAG-----781
Qy      257 ArgArg***AsnGlyGlu*****GlnGlyGlu***SerGlyVal***Leu---AspThr 275
Db      782 -----GAGAAGAAAGACCGCGAGTTCGAGCGACGACATCGTCGACGT 826
Qy      276 LeuLeuGlnPheAlaGluAspGlnThr**GlnIleLysIleThrLys*****Ile*** 295
Db      827 CTTTTCAGATGACAGAAAGGCGACGACATCAAAATTCCTTCAATTCATTCATCAG 886
Qy      296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGlnTrp 315
Db      887 GGTTCATTTTCGACACCTTCTCCGGGAGCTGAACGTCCTTCGACGACCATCTCATGG 946
Qy      316 AlaLeuAlaGluLeuIleAsnAsnPro***ValIleu*****AlaArgGlnGlu***Ty 335
Db      947 GCGTTTCCGAATCTGATGAGGAATCCGCGAAGATGCGCAAGTCCAGCGGAGCGTAAGA 1006
Qy      336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyIle 355
Db      1007 GAGCGCTCAAGGAAAGACAGTCGTGATTTGAGCGAGGTGCAAGCATCAAAATACCTG 1066
Qy      356 ArgAlaIleValLysGlnThrPheArgMetHisPProProleuProValValLysArglys 375
Db      1067 AGATCGGTGTTAAAGAGACTGAGGCTGACCCCTCCCTTCATTAAATCCCAAGACAA 1126
Qy      376 Cys**GluGlnCys***IleAsnGly**Val***ProGlnGlyAlaIleu*****Phe 395
Db      1127 TCCAGGGAAGAAATCCAGAGTTAAAGGGTACACGATTCGCGCAAAACTAATACTTCATC 1186
Qy      396 AsnValIleGlnIleValGly***Asp***LysTyTrpAspArgProSerGln***ArgPro 415
Db      1187 AACGTCTGGGCTATCCGAAGAGATCCCAATATCTGGGAAGATCCCGACACTTCGCGCT 1246

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Qy      416 GluArgPheLeuGlnThr***AlaGlnGlyGluAla*****LeuAspLeuArgly*** 435
Db      1247 GAGAGATTCGATGAGAGGTTTCCAGG-----GATTTCATGGGAAC 1285
Qy      436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
Db      1286 GATTCGAGTTCATCCCATTCGAGGCGGATCGAAGAAATCGCCCGTTTACATTTCCGG 1345
Qy      456 ThrSerGly***AlaThrIleuAlaSerLeuIleGlnCysPheAspLeuGlnValIleu 475
Db      1346 CTGGCAATAGTTAGATCCCATTTGGCGCAACTGCTTACACTTGCATCGAAATTG--- 1402
Qy      476 GlyProGlnGlyGlnIleuLysGly***AspAlaLysValSerMetGlnGluArgAla 495
Db      1403 ---CCACAAGAAATG-----ACTGATCCGACTTGGACATGACGAGACCCCA 1447
Qy      496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
Db      1448 GGTCTTCTGGGCAAAAAGAAATGTTTGTCTGTGCC 1489

RESULT 12
US-09-292-768-65
; Sequence 65, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Dupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: wslr13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; EARLIER FILING DATE: 1999-04-14
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-6-hydroxylase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1762)
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
; US-09-292-768-65

Alignment Scores:
Pred. No.: 6,98e-75 Length: 1762
Score: 618.50 Matches: 146
Percent Similarity: 48.38% Conservative: 93
Best Local Similarity: 29.55% Mismatches: 214
Query Match: 25.89% Indels: 41
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-292-768-65 (1-1762)
Qy      26 SerLYAlaLeuArgHisIleuProAsnProProSerPro***ProArgLeuProPheIle 45
Db      101 TCGAAATCCCAACAAACCTA-----CCTCGAGGCGCT---CCGAAGCTGGCGGTGATC 151
Qy      46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyAla***IleAspLeuSerLys 65
Db      152 GGCACCTCCACTTCTGTGGGAGGCGTTCCCCAGACGTTTGAAGACATAGCCCAAG 211

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QY 66 LysHISgLYProleuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
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   |||
Db 212 AAGTACGGGCGCGGTGCGACGTCGACGTCGGAGAGTACTGCTGCTGTGTGCGTGC 271
   |||
   |||
   |||
QY 86 ProGluLeuPheLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
   |||
   |||
   |||
Db 272 GCGGAGGACAGGAGGCGGATGAGTGGCTGAC---CCGAACTTCGCCAGCCGGTTC 328
   |||
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QY 106 GlnThrSerAla***Arg***LeuThrIYAsp-----ValAla*****Pro*** 124
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Db 329 GAGGCGATCGGCTCCAGGACCATGTGTAGACAAAGATGATCATCTTCACCCCTTAC 388
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QY 125 GlyProTyTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThrThr 144
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Db 389 AACGATCACTGGCGCGCATGCGAGGATCTGCGTGCAGAGCTGCTGAGCCCGAAGAAC 448
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QY 145 ValAsn***LeuArgProleuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
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Db 449 GTCAGGTCTTCGAGTACATGACATGACAGAGAGATGACGCTCATCCGGCTGCGG 508
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QY 165 Gln***AlaGluAla***LysProleuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
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Db 509 TCCTCGGGGGAGCG---CCGCTGACGTGACGAGAGAGGTCTGCAAGATGTGCTGT 562
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QY 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
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Db 563 GTGCTGTCTGTCAGAGCGCGGCTTCGGAGTGTGCTGACAGACAGAGGTTGTCGGAG 622
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QY 201 IleAlaArgGluValLeuLysIle***GlyGluTrpSerIleThrAspPheIle***Pro 220
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Db 623 TTGGTGAAGAGTGTGCTGATTCGCTCGCGGTTTTCAGCTGCGGAGT---CTCTACCT 679
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QY 221 -----LeuLys***LeuLysValGlyLysTrpGluLysArgIleAspPheIle 236
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Db 680 TCCTCATGTCTCTCAACCTGCTTACGCTTGAACAAGTAC-----AGTTCGACAGAGAT 733
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QY 237 LeuAsnLysPheAspProValIleGluArgValIleLysLysArgArg***IleValArg 256
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Db 734 CGCCGCGCTCATCATCATCTTTCGATGGGTCTCGAGAGCATGAG----- 781
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QY 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
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Db 782 -----GAGAAGAAAGAGCGCGAGTTTGAGCGAGCATCTGTGACGCTT 826
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QY 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
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Db 827 CTTTTCAGATGACAAAGGCGAGCATCAAAATTCCTTACTTCCATTCATGATCAG 886
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QY 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
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Db 887 GGTTCATTTTCGACACCTTCTCCGCGGAGCTGAAAGCTTTCGACGACCATCTCATGG 946
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QY 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
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Db 947 GCGTTCGGAACGATGAGAGATCCGCGCAAGATGCGCAAGTGCAGGCGAGAGTAA 1006
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QY 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyIle 355
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Db 1007 GAGCGCGCTCAAGGAAAGACAGCTGTGATTTGAGCGAGTGCAGAGCTTCAAAATCTCTG 1066
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QY 356 ArgAlaIleValLysGluThrPheArgMetHisProProleuProValValLysArgLys 375
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Db 1067 AGATTCGCTTAAAGAGACTCTGAGGCTGCACCTCTTTCATTAATCCAAAGACAA 1126
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QY 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
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Db 1127 TCCAGGGAAGATGAGGATTAACGGGTACACGATTCGCGCAAAATGATCTTCATC 1186
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QY 396 AsnValITPGLInValGly***Asp***LysTyTrpPAPArgProSerGlu***ArgPro 415
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Db 1187 AACGTCTGGCTATCGGAAGGATCCCAATATCTGGGAAGATCCGACACCTTCGCGCT 1246

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QY 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
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QY 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
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Db 1286 GATTTCGAGTTTCATCCATTCGCGGCGGCTCAGAAATCTGCCGCTTACATTTCCGG 1345
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QY 456 ThrSerGly***AlaThrLeuLeuAlaSerIleGlnCysPheAspLeuValLeu 475
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Db 1346 CTGGCAATGTGAGATCCCATTTGGCGACACTGCTTACCACTTCGATCGGAATTC--- 1402
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QY 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
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Db 1403 ---CCAAAGAAATG-----ACTGATGCCACTTGAGATGACGAGACCCCA 1447
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QY 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
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Db 1448 GGTCTTTCGGGCCAAAGAAATGTTCTGTTCC 1489

RESULT 13
US-09-351-229-3
; Sequence 3, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; EARLIER FILING DATE: 1999-07-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Zea mays
US-09-351-229-3

Alignment Scores:
Pred. No.: 8 51e-75 Length: 1806
Score: 618.00 Matches: 164
Percent Similarity: 50.40% Conservative: 90
Best Local Similarity: 32.54% Mismatches: 199
Query Match: 25.87% Indels: 52
DB: 3 Gaps: 13

US-09-857-581b-66 (1-521) x US-09-351-229-3 (1-1806)
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QY 55 LeuLeuHisTyTrpAla***IleAspLeuSerLysLysHisGlyProleuPheSer***** 74
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Db 140 CTGCCCAACGCTCCAGAACGAGCTCTCCAAAGCGGTACGTCGCTCATGACGCTCTG 199
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QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuLeuGln 94
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Db 200 TTGGGCTGTGCTGCTGTGTGTCGCGCGCTCCGCGAGATGGCAAGACTTCTCTCAG 259
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QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
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Db 260 ACCAAGACAGCG---GGTCTCCGACCGGCGGAGTTCGACAGTCGCGCAAGTACACCGCG 316
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QY 115 TyTrp---*****ValAla*****Pro***GlyProTyTrp***PheValArgLys 133
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Db 317 TACACATGCTCCGCGCTTCTGTGGCTCTTTTGAGCGGTACCTGCGCCAGGACGCGAGG 376
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QY 134 LeuIleMetAsnAspLeu***AsnAlaThrValAsn***LeuArgProleuArgThr 153
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Db      181 CTGCCGACGACCGCTGGCCAGCGTGGCGAAGCAGTCCGCGCAGTGGCGACGTGGCAG 240
Qy      75 PheGlySerMetProThrValValAlaIleSerThrProGluLeuPheLeuPheLeuGln 94
Db      241 CTGGGAGAGGTGTTCTCCGTGCTCTGCTCCCGGAGGCGACGAAAGAGGAGGATGAG 300
Qy      95 ****GluAlaIleTherPhe****ThrArgPheGlnTherSerAla****Arg****LeuThr 114
Db      301 CTGGTGGAC---CCGGCTGCGCGGACCGGTTCGAGAGCATCGGAGCATCATGATGTGG 357
Qy      115 TyrAsp---****ValAla****Pro****GlyProTyrTrrp****PheValArgIys 133
Db      358 TAGGACAAACGACGACATCATCTTCAGCCCTACAGCGCTGACCTGGCGCGAGATGCGGAG 417
Qy      134 LeuIleMetAsnAspLeu****AsnAlaIleThrValAsn****LeuArgProLeuArgThr 153
Db      418 ATCTGCTCTCCGACCTCTCAGCGCCGCGACGCTCCGCTCTTGGCTTCATCAGGACG 477
Qy      154 GlnGlnIleArgIys****LeuArg****MetAlaGln****AlaGluAla****LysProLeu 173
Db      478 GACGAGGTGTCCTCCGCTCTCGGCGACCTCGGCTCCGCGCGGCGGAGGCGCGTGG 537
Qy      174 Asp****ThrGluLeuLeuLeuLysTrrp****AsnSerThr****SerMetMet****LeuGly 193
Db      538 GACCTCAGGAGCGGATAGCGAGCGCTGACGCTGCTCATCTGACAGGCGCGCGTTCGG 597
Qy      194 -----GluAlaGlnGlnIleArgAspIleAlaArgGluValLeuLysIle**** 209
Db      598 AGCGTGATCAGGACGACGAGAGAGCTGTGTGAGTGTGTAAGGAGCGCTTCAGCATGGC 657
Qy      210 GlyIuTyrSerLeuThrAspPheIle****ProLeuLys****Leu----- 224
Db      658 TCCGGGTTCAGAGCTCGCGGACATGTTCCCTCCCAAGCTCCCACTTCGCTGCTGG 717
Qy      225 -----LysValIleLysTyrGluLysArgIleAspIleLeuAsnLysPheAsp 241
Db      718 AACAGAGCAAGCTGTGAGAGATGCGCGCGCTGACGCGCATCTCGAGGCGCATC--- 774
Qy      242 ProValValGluArgValIleLysLysArgArg****IleValArgArgArg****AsnGly 261
Db      775 ---GTGAGAGACCAAGCTCAGAG--- 798
Qy      262 Glu*****GluGlyGlu*****SerGlyVal-----LeuAspThrLeuLeuGluPheAla 280
Db      799 -----ACGGCGAGCTTGGCGCGGAGACATTTATGACGTAATCTTTAGATGAG 849
Qy      281 GluAspGluThr****GluIleLysIleThrLys****Ile****GlyLeuValValAsp 300
Db      850 AAGATAGCCAGATCAAAATCCCATCCACACCAAGCGCATCAAAAGCTTCATCTTCGAC 909
Qy      301 ****PheSerAlaGly****AspSerThrAla****ThrGluTrrpAlaLeuAlaGluLeu 320
Db      910 ACGTTCTCAGCGGAGACGAGCATCATCAACCAACCATCTGTGGTGTGAGCGAGTGG 969
Qy      321 IleAsnAsnPro****ValLeu****AlaArgGluGlu****TyrSerValValIleGlyLys 340
Db      970 ATGAGGAAATCCAGAGGTATGATCGCAAAAGCGAGCGAGCGGCGCTGAAGGCG 1029
Qy      341 Asp****LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValIys 360
Db      1030 AAGACGAGCTGGAGCTGAGACGAGCATGAGAGGCTTAATGATCAATGAAATCGGTGTGAG 1089
Qy      361 GluThrPheArgMetHisProProLeuProValValLysArgIysCys****GluGluLys 380
Db      1090 GAGAGGATGAGAGATGACCTCTCCGATCCGTTGATCCGAGATCATGACAGAGAAATGTC 1149
Qy      381 ****IleAsnGly****Val****ProGluGlyAlaLeu****PheAsnValTrrpGlnVal 400
Db      1150 GAGGTCAACGGGTACAGATTCGAAATAAGGCAAGATCATGATCAAGTGTGGTCCATG 1209
Qy      401 Gly****Asp****LysTyrTrrpAspArgProSerGlu****ArgProGluArgPheLeuGlu 420
Db      1210 GGTAGGAATCTCTCTACTGGGAAAAAACCCGAGACCTTTTGGCCCGAAAGGTTT----- 1263

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Qy      421 Thr****AlaGluGlyGluAla*****LeuAspLeuArgIys****HisPheGlnLeuLeu 440
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Qy      441 ProPheGlySerGlyVal****MetCysProGlyVal****LeuAlaIleSerGly****Ala 460
Db      1309 CCAATTGGAGCTGGAAAGAAATTCGCGCGGTTCATTTTCGGGTTCGCAATGTTGAG 1368
Qy      461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
Db      1369 GTCCATTGGCACAGCTTCTTACACACTTCGACGTGAGATGGCGGAGAAATGAACCT 1428
Qy      478 GlnGlyGlnIleLeuLysGly****AspAlaLysValSerMetGluLysArgAlaGlyLeu 497
Db      1429 -----TCCGATATGACATCTGTGAGCGAAGAGGCTTT 1461
Qy      498 ThrValProArgAlaHisSerLeuValCysValPro 509
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RESULT 15
US-09-292-768-3
; Sequence 3, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: wsur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; EARLIER FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Mentha piperita
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1518)
US-09-292-768-3

Alignment Scores:
Pred. No.: 1,216-74 Length: 1665
Score: 616.50 Matches: 145
Percent Similarity: 47.76% Conservative: 90
Best Local Similarity: 29.47% Mismatches: 206
Query Match: 25.81% Indels: 51
DB: Gaps: 11

US-09-857-581B-66 (1-521) x US-09-292-768-3 (1-1665)
Qy      35 ProProSerPro****ProArgLeuProPheIleGlyHis****HisLeuLeuLysAspLys 54
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Qy      55 LeuLeuHisTyrAla****IleAspLeuSerLysIleSgLYProLeuPheSer***** 74
Db      181 CTGCCGACGACGCGGTGCGCGAGGTGCGCAAGCATGACGCGCCAGTGGCGCACGTGCAG 240
Qy      75 PheGlySerMetProThrValValAlaIleSerThrProGluLeuPheLysLeuPheLeuGln 94
Db      241 CTGGGAGAGGTGTTCTCCGTGCTCTGCTCCCGGAGGCGACGAAAGAGGAGGATGAG 300
Qy      95 ****GluAlaIleTherPhe****ThrArgPheGlnTherSerAla****Arg****LeuThr 114
Db      301 CTGGTGGAC---CCGGCTGCGCGGACCGGTTCGAGAGCATCGGAGCATCATGATGTGG 357

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QY 115 TyrAsp-----ValAla*****Pro***GlyProHyTrp***PheValArgLys 133
 DB 358 TACGACAAAGACACATCATCTTACAGCCCTTACAGCGTCGACCTGGCGCCAGATGCGAAG 417
 QY 134 Leu1IleMetAsnAspLeu***Asn1ArhTrhValAsn***LeuArgProLeuArgTrh 153
 DB 418 ATCTGGCTCTCCGAGCTCTCCAGCGCCGCGACGTCGCTCTTCCGGCTTACAGGCGAG 477
 QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGlnAla***LysProLeu 173
 DB 478 GACGAGGTGTCCGCTCTCCGCGCACCTCCGCTCTCCGCGCGCGCGGCGCGCGCTG 537
 QY 174 Asp***ThrGlnGlnIleuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
 DB 538 GACCTCAAGAGCGGATGAGGACGCTGACGCTGCTCACTCTGCGAGGGGCGGCTTCGG 597
 QY 194 -----GlnAlaGlnGlnIleArgAsp1IleAlaArgGlnValLeuLysIle*** 209
 DB 598 AGCGTGATCAGGAGCACGACGAGGAGCTGTGTGAGCTGTGTAAGAGCGCCTCAGCATGGCG 657
 QY 210 GlyGlnTrpSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
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 QY 225 -----LysValGlyLysTrpGlnLysArg1IleAspAsp1IleLeuAsnLysPheAsp 241
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 QY 281 GlnAspGlnThr***GlnIleLys1IleThrLys*****Ile***GlyLeuValValAsp 300
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 QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGlnTrpAlaLeuAlaGlnLeu 320
 DB 910 ACCTTCTCAGCGGAGCCGAGCATCATCAACACGACCTCGTGGGTGATGGCGAGCTG 969
 QY 321 IleAsnAsnPro***ValLeu*****AlaArgGlnGln***TyrSerValValGlyLys 340
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 QY 341 Asp***LeuValAspGlnValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
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 QY 401 Gln***Asp***LysTrpTrpAspArgProSerGln***ArgProGlnArgPheLeuGln 420
 DB 1210 GGTAGGATCTCTCTCTATGTGGAAGAACCCGAGACCTTTGGCCCGAAGGTTT----- 1263
 QY 421 Thr***AlaGlnGlnGlnAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 DB 1264 -----GACCAAGTCTCGAGGAGATTTCATGTGGAAGAAAGATTTGAGTTTCATC 1308
 QY 441 ProPheGlnSerGlyArg***MetCysPProGlyVal***LeuAlaTrpSerGly***Ala 460
 DB 1309 CCATTTGAGCTGTGAAGAAAGATCTGCCCCGCTTTCGGAATTTTCGGGTTTGCAAAATGTTGAG 1368
 QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477

DB 1369 GTCCATTGGCACAGCTTCTTTACCACTTGCAGCTGGAAGTTGGCGGAAGAAATGAACCTT 1428
 QY 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGlnGlnArgAlaGlyLeu 497
 DB 1429 -----TCCGATATGACATGTCTGTAGGACAGAAAGGCTTT 1461
 QY 498 ThrValProArgAlaHisSerLeuValCysValPro 509
 DB 1462 ACCGGAATTAAGAAAGACATCTTCTACTGTTCCC 1497

Search completed: December 22, 2005, 00:21:08
 Job time : 291 secs